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OM protein - protein search, using sw model

Run on: April 20, 2006, 09:57:29 ; Search time 188 Seconds
(without alignments)
70.114 Million cell updates/sec

Title: US-10-666-423-1
Perfect score: 162
Sequence: 1 DAERFHDSGYEVHHQKLVFPAEDYGSNKGKGA 30

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq. 21: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	30	2	AAW81468 Synthetic
2	162	100.0	30	5	AAU11766 Human amy
3	162	100.0	30	6	ABR42769 Human amy
4	162	100.0	30	7	ADK82701 Beta-amy1
5	162	100.0	30	8	ADK35870 Human amy
6	162	100.0	30	9	AD259196 Human amy
7	162	100.0	32	8	ADP73486 Alzheimer
8	162	100.0	33	2	AAW81469 Synthetic
9	162	100.0	33	5	AAU93990 Human bet
10	162	100.0	33	7	ADK10851 Chimeric
11	162	100.0	33	7	ADK39756 B-cell pe
12	162	100.0	33	8	ADG63951 Recombina
13	162	100.0	33	8	ADP73485 Alzheimer
14	162	100.0	33	8	ADK12778 Human bet
15	162	100.0	35	2	AAW47228 Beta-amy1
16	162	100.0	35	6	AAE35430 Vaccine a
17	162	100.0	35	6	ADQ37254 Abeta pep
18	162	100.0	36	2	AAW81471 Synthetic
19	162	100.0	36	5	AAU11776 Synthetic
20	162	100.0	36	5	AAU11771 Synthetic
21	162	100.0	36	6	ABR42779 Amyloid b
22	162	100.0	36	6	ABR42774 Amyloid b
23	162	100.0	36	8	ADP73823 Loop inhe
24	162	100.0	38	2	AAW60362 Beta-amy1

25	162	100.0	38	2	AAW92722 Human tae
26	162	100.0	38	4	AAW91826 Amyloid b
27	162	100.0	38	4	AAW91799 Amyloid b
28	162	100.0	38	9	ADY81762 Human bet
29	162	100.0	39	2	AAW60363 Beta-amy1
30	162	100.0	39	2	AAW81472 Synthetic
31	162	100.0	39	2	AAW25134 Human amy
32	162	100.0	39	6	ABU08509 Human amy
33	162	100.0	39	6	ADP96148 Human Abe
34	162	100.0	39	9	ADY81763 Human bet
35	162	100.0	40	2	AAW33191 Beta-amy1
36	162	100.0	40	2	AAW60364 Beta-amy1
37	162	100.0	40	2	ADK11651 Human bet
38	162	100.0	40	2	AAW23335 Amyloid b
39	162	100.0	40	2	AAW37507 Amyloid b
40	162	100.0	40	2	AAW47226 Beta-amy1
41	162	100.0	40	2	AAW14099 Human bet
42	162	100.0	40	2	AAW39804 Beta-amy1
43	162	100.0	40	2	AAW99584 Wild type
44	162	100.0	40	2	AAW81473 Synthetic
45	162	100.0	40	2	AAW39339 Beta-amy1
46	162	100.0	40	2	AAW25135 Human amy
47	162	100.0	40	2	AAW92723 Human tae
48	162	100.0	40	4	AAW84426 Partial s
49	162	100.0	40	4	AAW91813 Amyloid b
50	162	100.0	40	4	AAW91780 Amyloid b
51	162	100.0	40	4	AAW91829 Amyloid b
52	162	100.0	40	4	AAW91802 Amyloid b
53	162	100.0	40	4	AAW05483 Human pep
54	162	100.0	40	5	AAW99425 Human amy
55	162	100.0	40	5	AAW22990 Human amy
56	162	100.0	40	5	AAU11773 Synthetic
57	162	100.0	40	5	AAU11772 Synthetic
58	162	100.0	40	5	AAW68313 Human bet
59	162	100.0	40	5	AAU96895 Human sel
60	162	100.0	40	5	AAW50909 Beta amy1
61	162	100.0	40	5	AAW80186 Amyloid b
62	162	100.0	40	5	AAE26332 Human bet
63	162	100.0	40	5	AAW51863 Human amy
64	162	100.0	40	6	ABU08710 Amyloid b
65	162	100.0	40	6	ABU08508 Human amy
66	162	100.0	40	6	AAO19885 Human amy
67	162	100.0	40	6	ABP96147 Human Abe
68	162	100.0	40	6	AAE35429 Abeta pro
69	162	100.0	40	6	ABP60626 Human A-b
70	162	100.0	40	6	ABP97883 Amino aci
71	162	100.0	40	6	ABR42775 Amyloid b
72	162	100.0	40	6	ABR42776 Amyloid b
73	162	100.0	40	6	ABU63706 Rat amy1o
74	162	100.0	40	7	ADA37266 Human bet
75	162	100.0	40	7	ADB85563 Beta-amy1
76	162	100.0	40	7	AAE38648 Human amy
77	162	100.0	40	7	ADG66001 Human A(b
78	162	100.0	40	7	ADG35182 Beta-amy1
79	162	100.0	40	7	ADT55648 Human A b
80	162	100.0	40	7	ADK82702 Beta-amy1
81	162	100.0	40	8	ADP53270 Amyloid A
82	162	100.0	40	8	ADN00693 A40, SEO
83	162	100.0	40	8	ADN41885 Amino aci
84	162	100.0	40	8	ADN41881 Amino aci
85	162	100.0	40	8	ADN41882 Amino aci
86	162	100.0	40	8	ADN41884 Amino aci
87	162	100.0	40	8	ADN41865 Amino aci
88	162	100.0	40	8	ADN41880 Amino aci
89	162	100.0	40	8	ADN01000 Human bet
90	162	100.0	40	8	ADQ26239 Human amy
91	162	100.0	40	8	ADQ37253 Vaccine a
92	162	100.0	40	8	ADK16410 Human Abo
93	162	100.0	40	8	ADK16410 Human Abo
94	162	100.0	40	8	ADU24434 Novel glu
95	162	100.0	40	8	ADU46708 Amyloid b
96	162	100.0	40	9	ADV50991 Alzheimer
97	162	100.0	40	9	ADW38388 Human bet

98	162	100.0	40	9	ADY72249	N-termina
99	162	100.0	40	9	ADY81764	Human bet
100	162	100.0	40	9	ADY78385	Human amy

ALIGNMENTS

RESULT 1
AAW81468 standard; peptide; 30 AA.

AAW81468;

28-JAN-1999 (first entry)

Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30) .

KM Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KM research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PN US5840838-A.

PD 24-NOV-1998.

PR 29-FEB-1996; 96US-00609090.

PR 29-FEB-1996; 96US-00609090.

(KENT) UNIV KENTUCKY RES FOUND.

PI Aksekov M, Carney JM, Hensley K, Butterfield DA;

WPI; 1999-034120/03.

PT Process for treating synthetic amyloid beta peptides - by organic solvent
PT treatment; useful for studying neurotoxicity.

PS Claim 5; Col 9-10; 14pp; English.

CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic Abeta
CC peptide that comprises dissolving the peptide in a deoxygenated solvent
CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution
CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative
CC deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful
CC as research tools for studying neurotoxicity resulting from Abeta peptide
CC -enhanced free-radical production. The treatment increases the activity
CC of the synthetic Abeta peptides in tests to determine free-radical
CC generating capacity and glutamine synthetase inactivation

SQ Sequence 30 AA;

Query Match 100.0%; Score 162; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKG	30
DB	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKG	30

RESULT 2
AAU11766 standard; protein; 30 AA.

AAU11766;

26-MAR-2002 (first entry)

XX	Human amyloid beta protein 1-42, amino acids 1-30.
DE	Amyloid beta; non-amyloidogenic peptide; vaccine; immunogen;
XX	Alzheimer's disease; amyloid fibril; human.
KW	Homo sapiens.
XX	WO200190182-A2.
XX	29-NOV-2001.
XX	22-MAY-2001; 2001WO-US016322.
XX	22-MAY-2000; 2000US-0205578P.
XX	(UYNY) UNIV NEW YORK STATE.
XX	Frangione B, Wisniewski T, Sigurdsson EM;
XX	WPI; 2002-106186/14.

PT Novel isolated synthetic immunogenic but non-amyloidogenic peptide
PT homologous to amyloid beta, useful for inducing immune response to
PT amyloid beta peptides and amyloid deposits.

PS Claim 1; Page 62; 69pp; English.

CC The invention relates to an isolated synthetic immunogenic but non-
CC amyloidogenic peptide homologous to amyloid beta. The peptide may be
CC conjugated to polymer molecule. Antibodies raised against the peptide
CC are also included. The peptide is useful for inducing an immune response
CC to amyloid beta peptides and amyloid deposits and therefore treating
CC Alzheimer's disease. The antibody is useful for reducing the formation of
CC amyloid fibrils and deposits. The peptide has a reduced ability to adopt
CC a beta-sheet confirmation as an antigenic source, and a much lower risk
CC of leading to any toxic effects in humans. The present sequence is a
CC human amyloid beta 1-42, residues 1-30 which is used as a basis for the
CC peptides of the invention

SQ Sequence 30 AA;

Query Match 100.0%; Score 162; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKG	30
DB	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKG	30

RESULT 3
ABR42769 standard; peptide; 30 AA.

ABR42769;

08-SEP-2003 (first entry)

Human amyloid beta(1-42) amino acid residues 1-30.

XX Human amyloid beta; amyloidosis; Alzheimer's disease; nootropic;
KW neuroprotective; immunogen; vaccine.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..11 "major immunogenic site of amyloid beta"

FT Region 22..28 "major immunogenic site of amyloid beta"

XX WO2003045128-A2.

XX 05-JUN-2003.
 PD
 XX
 PF 21-NOV-2002; 2002WO-US037634.
 PR 21-NOV-2001; 2001US-0331801P.
 XX
 PA (UTNY) UNIV NEW YORK STATE.
 XX
 PI Frangione B, Wisniewski T, Sigurdson EM;
 XX
 DR WPI; 2003-505145/47.
 XX
 PT New synthetic immunogenic but non-deposit forming peptides, useful for
 PT inducing an immune response to prions, amyloids, amylin or amylin
 PT fibrils, particularly for treating e.g. Alzheimer's, scrapie or
 PT Creutzfeldt-Jacob disease.
 XX
 PS Claim 1; Page 210; 265pp; English.
 XX
 CC The present sequence comprises amino acid residues 1-30 of the amyloid
 CC beta(1-42) protein. The invention provides a synthetic immunogenic but
 CC non-amyloidogenic peptide homologous to this sequence, where 0-5 of
 CC hydrophobic residues 17-21 are substituted with Lys, Asp, Glu, Pro, Gly
 CC or Ser, and preferably also include an N-terminal and/or C-terminal
 CC segment of 4-10 Lys or Asp residues. Preferred peptides are given in
 CC ABR42770-73, ABR42777-78 and ABR42783-88. The peptides, alone or
 CC conjugated to an immunostimulant, are used to induce an immune response
 CC to amyloid beta peptides, and immunizing compositions comprising the
 CC peptides are used in a claimed method of reducing amyloidosis. Antibodies
 CC directed against the peptides can be used in passive immunization
 XX
 SQ Sequence 30 AA;

Query Match 100.0%; Score 162; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 4
 ADK82701
 ID ADK82701 standard; peptide; 30 AA.
 XX
 AC ADK82701;
 XX

DT 06-MAY-2004 (first entry)

DE Beta-amyloid peptide #7 recognised by antibody to treat senile dementia.

KW fusion antibody; senile dementia; beta-amyloid peptide; fibre;

KW immunocell.

OS Homo sapiens.

XX
 PN CN1396183-A.
 XX

PD 12-FEB-2003.

XX 13-JUL-2001; 2001CN-00120278.
 PF

XX 13-JUL-2001; 2001CN-00120278.
 PR

XX (ZHAN/) ZHANG X.
 PA

PI Zhang X, Zhang J;
 XX

DR WPI; 2003-442233/42.
 XX

PT Human fusion antibody for reducing cerebral amyloid fibers associated

PT with senile dementia.
 XX
 XX Claim 1; Page 2; 26pp; Chinese.
 XX

CC The invention relates to a human fusion antibody for preventing and
 CC treating senile dementia. The antibody recognises and binds the beta-
 CC amyloid peptide and the fibres generated by it. The human antibody FC
 CC segment recognised by human immunocells are sequentially contained by its
 CC terminals from N to C. The fusion gene coding for the antibody is also
 CC disclosed. This sequence represents a beta-amyloid peptide recognised by
 CC the antibody.
 XX
 XX

SQ Sequence 30 AA;

Query Match 100.0%; Score 162; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 5
 ADI35870
 ID ADI35870 standard; peptide; 30 AA.
 XX
 AC ADI35870;
 XX

DT 22-APR-2004 (first entry)

DE Amyloid beta peptide SEQ ID NO:24.

KW amyloid beta peptide; vaccine; immunisation; neuroprotective;

KW Alzheimer's disease.

OS Synthetic.

PN WO2004006861-A2.

PD 22-JAN-2004.

PF 16-JUL-2003; 2003WO-US022280.
 XX

PR 17-JUL-2002; 2002US-0396245P.
 XX

PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.
 XX

PI Chain DG, Fitzer-Atlas C;
 XX

DR WPI; 2004-122759/12.
 XX

PT New amyloid beta peptide, useful for preparing a composition for
 PT preventing the formation or progression of amyloid plaques for preventing
 PT or treating Alzheimer's disease.
 XX

PS Example 2; SEQ ID NO 24; 69pp; English.
 XX

CC The present invention describes an isolated amyloid beta peptide or its
 CC homologue which is selected by a method comprising: (a) determining the
 CC binding value of each amino acid of a subsequence of amyloid beta peptide
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)
 CC determining the resulting score of all amino acids of the subsequence,
 CC based on the binding value of each amino acid obtained in step (1); and
 CC (c) comparing the resulting score to a preselected value. Also described:
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,
 CC for immunisation of an individual based on the HLA haplotype of the
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta
 CC peptide to an individual based on the HLA haplotype of the individual;
 CC and (6) preventing the formation or progression of amyloid plaques. The

CC amyloid beta peptide has neuroprotective activity, and can be used in
CC vaccines. The amyloid beta peptide is useful for preparing a composition
CC for preventing the formation or progression of amyloid plaques for
CC preventing or treating Alzheimer's disease. The present sequence
CC represents an amyloid beta (Abeta) peptide, which is used in an example
CC from the present invention.
XX
SQ Sequence 30 AA;
Query Match 100.0%; Score 162; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
RESULT 6
ADZ59196 standard; peptide; 30 AA.
XX
XX ADZ59196;
XX
XX 14-JUL-2005 (first entry)
XX
XX Human amyloid beta peptide 1-30 SEQ ID NO:5.
XX
XX
XX blood-brain barrier; Alzheimer's disease; beta-amyloid.
XX
XX Homo sapiens.
XX
XX US2005095201-A1.
XX
XX 05-MAY-2005.
XX
XX 10-FEB-2004; 2004US-00775562.
XX
XX 29-OCT-2003; 2003US-0515460P.
XX
XX (PODU/) PODUSLO J F.
XX (CURR/) CURRAN G L.
XX (WENG/) WENGENACK T M.
XX (MCCO/) MCCORMICK D J.
XX (FAUQ/) FAUQ A H.
XX
XX Poduslo JF, Curran GL, Wengenack TM, McCormick DJ, Fauq AH,
XX WPI; 2005-344974/35.
XX
XX Amino acid composition, useful in molecular imaging, comprises a
XX chemically synthesized amino acid polymer comprising at least one
XX asparagyl-4-aminobutane or glutamyl-4-aminobutane residue.
XX
XX Example; SEQ ID NO 5; 24pp; English.
XX
XX The invention relates to an amino acid composition (1), with improved
XX blood brain barrier permeability, comprising a chemically synthesized
XX amino acid polymer comprising at least one asparagyl-4-aminobutane or
XX glutamyl-4-aminobutane residue. Also described: (1) creating an amino
XX acid polymer with improved blood brain barrier permeability comprising
XX chemically synthesizing an amino acid polymer (where at least one
XX asparagyl-4-aminobutane or glutamyl-4-aminobutane residue is incorporated
XX within the amino acid polymer); (2) a product of (1); and (3)
XX synthesizing N-alpha-Fmoc-L-aspartyl-alpha-(4-aminobutyl)-carbamic acid
XX tert-butylester or N-alpha-Fmoc-L-glutamyl-delta-(4-aminobutyl)-carbamic
XX acid tert butyl ester. (1) is useful in medical imaging diagnostic
XX procedures. (1) is useful as a therapeutic agent or as an agent used in
XX molecular imaging. (1) is useful in therapies that require the delivery
XX of a peptide or polypeptide across the blood brain barrier. (1) is useful
XX in the diagnosis or detection of Alzheimer's disease (7) is useful in
XX the detection of amyloid plaque in Alzheimer's disease patients. The
XX present sequence represents human amyloid beta peptide 1-30, which is

CC used in the exemplification of the present invention.
XX
XX Sequence 30 AA;
SQ
Query Match 100.0%; Score 162; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
RESULT 7
ADP73486 standard; peptide; 32 AA.
XX
XX ADP73486;
XX
XX 09-SEP-2004 (first entry)
XX
XX Alzheimer's disease B cell epitope of gene beta-amyloid, SEQ ID 99.
XX
XX transgenic animal; Hepatitis B virus nucleocapsid core protein; HBC;
XX enhanced stability; hepatotropic; virocid; immunology;
XX protein engineering; immunogen; vaccine; Hepatitis B infection.
XX
XX Unidentified.
XX
XX WO2004053091-A2.
XX
XX 24-JUN-2004.
XX
XX 10-DEC-2003; 2003WO-US039164.
XX
XX 10-DEC-2002; 2002US-0432123P.
XX
XX (APOV-) APOVIA INC.
XX
XX Lyons K, Birkett AJ, Haron JA;
XX WPI; 2004-468859/44.
XX
XX New recombinant chimer hepatitis B core (HBC) protein molecules useful in
XX the fields of immunology and protein engineering, in particular as an
XX immunogen in a vaccine for Hepatitis B infections.
XX
XX Disclosure; SEQ ID NO 99; 338pp; English.
XX
XX The invention relates to a novel recombinant chimeric Hepatitis B virus
XX nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues
XX in length. The chimeric protein is engineered for both enhanced stability
XX of self-assembled particles and the substantial absence of nucleic acid
XX binding by the particles. The invention further comprises: a recombinant
XX HBC protein chimeric molecule that has a length of 135-365 amino acid
XX residues and contains four peptide-linked amino acid residue sequence
XX domains from the N-terminus that are denominated Domains I, II, III and
XX IV. The invention also provides nucleic acids, polypeptides, host cells,
XX vectors and transgenic animals used in the methods of the invention. The
XX chimeric compositions of the invention have hepatotropic and virocid
XX activities. The methods and compositions of the present invention are
XX useful in the fields of immunology and protein engineering, in particular
XX for using a chimeric hepatitis B virus nucleocapsid protein as an
XX immunogen in a vaccine for Hepatitis B infections. This sequence
XX represents a Hepatitis B virus nucleocapsid (core) protein related
XX polypeptide of the invention.
XX
XX Sequence 32 AA;
Query Match 100.0%; Score 162; DB 8; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 |||||
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 8
 AA081469
 ID AA081469 standard; peptide; 33 AA.
 XX
 AC AA081469;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).
 XX
 KM Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KM research; neurotoxicity; free-radical; glutamine synthetase.
 XX
 OS Synthetic.
 OS
 PN US5840838-A.
 XX
 XX 24-NOV-1998.
 PD
 XX 29-FEB-1996; 96US-00609090.
 PF
 XX 29-FEB-1996; 96US-00609090.
 PR
 XX 29-FEB-1996; 96US-00609090.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Aksenov M, Carney JM, Hensley K, Butterfield DA,
 XX WPI; 1999-034120/03.
 DR

XX Process for treating synthetic amyloid beta peptides - by organic solvent
 PT treatment, useful for studying neurotoxicity.
 XX
 PS Claim 5; Col 9-10; 14pp; English.
 XX

CC Sequences AA081466 to AA081476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic Abeta
 CC peptide that comprises dissolving the peptide in a deoxygenated solvent
 CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by "evaporative
 CC deposition" in 5-10 minutes. Synthetic amyloid beta peptides are useful
 CC as research tools for studying neurotoxicity resulting from Abeta peptide
 CC -enhanced free-radical production. The treatment increases the activity
 CC of the synthetic Abeta peptides in tests to determine free-radical
 CC generating capacity and glutamine synthetase inactivation
 CC
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 162; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 6.2e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 |||||
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 9
 AA093990
 ID AA093990 standard; peptide; 33 AA.
 XX
 AC AA093990;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human beta-amyloid B cell epitope #4.
 XX

KM Immunogenic; hepatitis virus nucleocapsid protein; hepatitis B core; HBC;
 KM vaccine; B cell epitope; T cell epitope; immunostimulant.
 XX
 XX Homo sapiens.
 OS
 XX WO200214478-A2.
 PN
 XX
 XX 21-FEB-2002.
 PD
 XX 16-AUG-2001; 2001WO-US041759.
 PF
 XX 16-AUG-2000; 2000US-0225843P.
 PR 22-AUG-2000; 2000US-0226867P.
 PR 15-AUG-2001; 2001US-00930915.
 XX
 PA (APOV-) APOVIA INC.
 XX
 XX Birkett AJ;
 PI
 XX WPI; 2002-257601/30.
 DR

PT Novel recombinant hepatitis virus nucleocapsid protein, termed as chimeric
 PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,
 PT HBC immunogenic loop with linker for conjugated epitope and C-terminus.
 PT
 XX
 PS Disclosure; Page 38; 28pp; English.
 XX

CC The invention relates to a recombinant hepatitis virus nucleocapsid protein,
 CC i.e. a chimeric hepatitis B core (HBC) protein (I), displaying one or
 CC more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or
 CC C-terminus, or having a heterologous linker for a conjugated epitope in
 CC (L), and containing a Cys residue at, or near, the C-terminus that
 CC confers enhanced stability to the particles. A vaccine comprising (I) is
 CC useful for inducing an immune response in an inoculated host animal, by
 CC inoculating a host animal with the vaccine, and maintaining that
 CC inoculated animal for a time period sufficient for that animal to develop
 CC an immune response. The immunogenic particles formed using (I) are
 CC substantially free of binding to nucleic acids, and are most stable than
 CC the particle formed from otherwise identical HBC chimera that lacks the C-
 CC terminal residue or in which a C-terminal Cys is replaced by another
 CC residue. The chimera particles are most stable on storage in aqueous
 CC compositions that are particles of similar sequence that lack any C-
 CC terminal Cys residues. The chimera molecule exhibits the self-assembly not
 CC exhibiting the nucleic acid binding of those native particles, and
 CC excellent B cell and T cell immunogenicities. The chimera particles are
 CC typically prepared in higher yield than similar particles that are free
 CC of a C-terminal Cys. The particles are often far more immunogenic than
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
 CC particles assembled from the chimera molecules are enhanced as compared to
 CC similar particles assembled from chimera molecules lacking at least one C-
 CC terminal Cys. AA093802-AA093997 represent immunogenic HBC particles amino
 CC acid sequences and related sequences of the invention
 CC
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 162; DB 5; Length 33;
 Best Local Similarity 100.0%; Pred. No. 6.2e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 |||||
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 10
 ADE10851
 ID ADE10851 standard; peptide; 33 AA.
 XX
 AC ADE10851;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Chimeric hepatitis B virus related B-cell epitope seqid 85.
 XX

XX hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;
XX recombinant hepatitis B core chimeric protein/HBc chimeric protein;
XX hepatitis B infection; T-cell stimulator; B-cell epitope.
XX
XX Unidentified.
XX
XX US2003198645-A1.
XX
XX 23-OCT-2003.
XX
XX 21-FEB-2003; 2003US-00372076.
XX
XX 21-FEB-2002; 2002US-00080299.
XX 21-FEB-2002; 2002US-00082014.
XX
XX (PAGE/) PAGE M.
XX (FRIE/) FRIEDE M.
XX
XX Page M, Friede M;
XX
XX WPI; 2003-852775/79.
XX
XX Treating chronic hepatitis B infection by administering a T cell-
XX stimulating vaccine containing immunogenic particles having recombinant
XX PT carboxy-terminal truncated hepatitis B core (HBc) chimeric protein
XX molecules.
XX
XX Disclosure; SEQ ID NO 85; 111pp; English.
XX
XX The invention describes a method of treating chronic hepatitis comprising
XX CC administering to a patient a T cell-stimulating amount of a vaccine
XX CC comprising immunogenic particles dissolved or dispersed in a diluent,
XX CC where the immunogenic particles consists of recombinant hepatitis B core
XX CC (HBc) chimeric protein molecules, and maintaining the patient to induce T
XX CC cells activated against HBc. The methods and compositions of the present
XX CC invention are useful for treating chronic hepatitis B infection. This is
XX CC the amino acid sequence of a chimeric hepatitis B virus related B-cell
XX CC epitope useful for expression within the HBV chimera at the N-terminus,
XX CC within the immunogenic loop and/or at the C-terminus.
XX
XX Sequence 33 AA;
XX
XX Query Match 100.0%; Score 162; DB 7; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 6, 2e-16; Mismatches 0; Gaps 0;
XX Matches 30; Conservative 0; Indels 0; Gaps 0;
XX
XX QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
XX 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
XX
XX Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
XX
XX RESULT 11
XX ADM39756 standard; peptide; 33 AA.
XX ID ADM39756;
XX AC ADM39756;
XX
XX 03-JUN-2004 (first entry)
XX
XX B-cell peptide epitope expressed by HBc chimera Seq 88.
XX
XX immunogenic; avian hepatitis B virus; nucleocapsid;
XX KW self assembled particle; immunogen; inoculum; vaccine; immunostimulant;
XX KW antibacterial; virucidal; B-cell epitope.
XX
XX Unidentified.
XX
XX OS US2003072722-A2.
XX PN 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005315.
XX
XX PF

XX 21-FEB-2002; 2002US-0359129P.
XX (APOV-) APOVIA INC.
XX
XX Birkett AJ, Peck B;
XX
XX WPI; 2003-679948/64.
XX
XX New recombinant chimera avian hepatitis B core protein molecule, useful as
XX PT an immunogen for inducing a B cell or T cell response to produce
XX PT antibodies, or as a vaccine against pathogens.
XX
XX Disclosure; SEQ ID NO 88; 278pp; English.
XX
XX This invention relates to novel recombinant immunogenic chimeric avian
XX CC hepatitis B core (AHBc) nucleocapsid proteins. Specifically, it refers to
XX CC an AHBc protein that has been engineered to display an immunogenic B cell
XX CC or T cell epitope, exhibit enhanced stability and an absence of nucleic
XX CC acid binding as a self assembled particle. The present invention
XX CC describes the chimeric AHBc protein as truncated at the C-terminus and
XX CC containing introduced cysteine residues that confers an enhanced
XX CC stability in aqueous solution, an increased yield and more immunogenicity
XX CC than similar conjugates that lack N- or C-terminal cysteines.
XX CC Furthermore, a reduction in the number of positively charged residues
XX CC (lysine and arginine) towards the C-terminus prepares self-assembled
XX CC particles that are substantially free of nucleic acid binding. As such,
XX CC these chimeric particles can be used as immunogens of an inoculum that
XX CC induce a B cell or T cell response in an animal to produce antibodies. It
XX CC can also be useful for developing a vaccine to protect against the
XX CC pathogen from which the heterologous epitope or the hapten is derived.
XX CC Accordingly, these compositions exhibit immunostimulant, antibacterial
XX CC and virucidal activities. This peptide sequence is an exemplary B-cell
XX CC epitope peptide immunogen useful for both linkage to the linker residue
XX CC after expression of a contemplated chimera and for expression within an
XX CC HBc chimera of the invention.
XX
XX Sequence 33 AA;
XX
XX Query Match 100.0%; Score 162; DB 7; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 6, 2e-16; Mismatches 0; Gaps 0;
XX Matches 30; Conservative 0; Indels 0; Gaps 0;
XX
XX QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
XX 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
XX
XX Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
XX
XX RESULT 12
XX ADG63951 standard; peptide; 33 AA.
XX ID ADG63951;
XX AC ADG63951;
XX
XX 11-MAR-2004 (first entry)
XX
XX Recombinant chimera hepatitis B core protein immunogenic epitope #76.
XX DE Recombinant chimera hepatitis B core protein; HBc; immunogenic epitope;
XX KW HBc immunodominant loop; immune response.
XX
XX Unidentified.
XX
XX OS US2003185858-A1.
XX PN 02-OCT-2003.
XX
XX 21-FEB-2002; 2002US-00082014.
XX PF 15-AUG-2001; 2001US-00930915.
XX
XX (BIRK/) BIRKETT A J.
XX
XX PA
XX
XX

PI Birkett AJ;
XX
XX WPI; 2004-031988/03.
DR
XX
XX Recombinant chimera hepatitis B core protein molecule useful for preparing
PT vaccine or inoculum includes peptide-bonded heterologous immunogenic
PT epitope at N-terminus in the hepatitis B core immunodominant loop or C-
XX terminus of the chimera.
XX
XX Disclosure; SEQ ID NO 84; 110pp; English.
XX
XX The invention relates to a recombinant chimera hepatitis B core (HBC)
CC protein molecule that includes a peptide-bonded heterologous immunogenic
CC epitope at the N-terminus in the HBC immunodominant loop or the C-
CC terminus of the chimera, or a heterologous linker residue for a conjugated
CC epitope present in the loop. The invention also relates to an immunogenic
CC particle comprising the recombinant hepatitis B core chimeric protein
CC molecule, a vaccine comprising the immunogenic particles dissolved or
CC dispersed in a diluent, a nucleic acid that encodes a recombinant HBC
CC protein molecule or its variant, analogue, or complement and a method for
CC inducing an immune response in an inoculated host animal comprising
CC inoculating a host animal with a vaccine and maintaining the inoculated
CC animal for a period of time sufficient to enable development of an immune
CC response. The recombinant chimera hepatitis B core protein molecule is
CC used in an immunogenic particle for preparing a vaccine useful for
CC inducing an immune response in an inoculated host animal. This sequence
CC represents an HBC protein immunogenic B cell epitope of the invention.
XX
XX Sequence 33 AA;
SQ
Query Match 100.0%; Score 162; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.2e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGA 30
DB 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGA 30
RESULT 13
ADP73485
ID ADP73485 standard; peptide; 33 AA.
XX
XX ADP73485;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Alzheimer's disease B cell epitope of gene beta-amyloid, SEQ ID 98.
DE
XX
XX transgenic animal; Hepatitis B virus nucleocapsid core protein; HBC;
KM enhanced stability; hepatotropic; virucide; immunology;
KM protein engineering; immunogen; vaccine; Hepatitis B infection.
XX
XX Unidentified.
OS
XX
XX WO2004053091-A2.
PN
XX
XX 24-JUN-2004.
PD
XX
XX 10-DEC-2003; 2003WO-US039164.
PF
XX
XX 10-DEC-2002; 2002US-0432123P.
PR
XX
XX (APOV-) APOVITA INC.
PA
XX
XX Lyons K, Birkett AJ, Haxon JA;
PI
XX
XX WPI; 2004-468859/44.
DR
XX
XX New recombinant chimera hepatitis B core (HBC) protein molecules useful in
PT the fields of immunology and protein engineering, in particular as an
PT immunogen in a vaccine for Hepatitis B infections.
XX

PS Disclosure; SEQ ID NO 98; 338pp; English.
XX
XX
XX The invention relates to a novel recombinant chimera Hepatitis B virus
CC nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues
CC in length. The chimera protein is engineered for both enhanced stability
CC of self-assembled particles and the substantial absence of nucleic acid
CC binding by the particles. The invention further comprises: a recombinant
CC HBC protein chimera molecule that has a length of 135-365 amino acid
CC residues and contains four peptide-linked amino acid residue sequence
CC domains from the N-terminus that are denominated Domains I, II, III and
CC IV. The invention also provides nucleic acids, polypeptides, host cells,
CC vectors and transgenic animals used in the methods of the invention. The
CC chimeric compositions of the invention have hepatotropic and virucide
CC activities. The methods and compositions of the present invention are
CC useful in the fields of immunology and protein engineering, in particular
CC for using a chimera hepatitis B virus nucleocapsid protein as an
CC immunogen in a vaccine for Hepatitis B infections. This sequence
CC represents a Hepatitis B virus nucleocapsid (core) protein related
CC polypeptide of the invention.
XX
XX Sequence 33 AA;
SQ
Query Match 100.0%; Score 162; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.2e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGA 30
DB 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGA 30
RESULT 14
ADRI2778
ID ADRI2778 standard; peptide; 33 AA.
XX
XX ADRI2778;
AC
XX
XX 04-NOV-2004 (first entry)
DT
XX
XX Human beta-amyloid protein B cell epitope #4.
DB
XX
XX Human; chronic hepatitis; HBC; nucleocapsid core protein; vaccine;
KM immunogen; immunogenic epitope; T cell; B cell; CD8+ cell; CD4+ cell;
KM cytotoxic T lymphocyte; toll-like receptor 4; toll-like receptor 9;
KM TLR-4; TLR-9; epitope.
XX
XX Homo sapiens.
OS
XX
XX US2004156863-A1.
PN
XX
XX 12-AUG-2004.
PD
XX
XX 01-OCT-2003; 2003US-00677074.
PF
XX
XX 21-FEB-2002; 2002US-00080299.
PR
XX
XX 21-FEB-2002; 2002US-00080214.
PR
XX
XX 21-FEB-2003; 2003US-00372076.
XX
XX (PAGE/) PAGE M.
PA (FRIE/) FRIEDE M.
PA (SCHM/) SCHMIDT A. E.
PA (STOB/) STOBBER D.
XX
XX Page M, Friede M, Schmidt AE, Stober D;
PI
XX
XX WPI; 2004-603322/58.
DR
XX
XX Treating chronic hepatitis, by administering vaccine comprising
PT immunogenic particles having recombinant hepatitis B core chimeric
PT protein molecules, that stimulates T cell, to patient chronically
PT infected with hepatitis B virus.
XX
XX Disclosure; SEQ ID NO 85; 117pp; English.
PS

XX The invention relates to treating chronic hepatitis, by administering a
 CC vaccine comprising immunogenic particles having recombinant hepatitis B
 CC core (Hbc) chimeric protein molecules (where truncated Hbc molecules are
 CC linked N-terminally or C-terminally to an immunogenic epitope), that
 CC stimulate T cell production, to a patient chronically infected with
 CC hepatitis B virus, and maintaining the patient for time sufficient to induce
 CC T cells activated against Hbc. The chimeric proteins are still capable
 CC self-assembling into particles upon expression in a host cell and are
 CC substantially free of binding to nucleic acids, and the particles display
 CC enhanced stability. Also included is enhancing (M2) the production of one
 CC or more of gamma-producing CD8⁺, CD4⁺ T cells and cytotoxic T lymphocytes
 CC against hepatitis B virus, involving administering to a patient
 CC chronically infected with hepatitis B virus, a T cell-stimulating amount
 CC of a vaccine comprising immunogenic particles dissolved or dispersed in a
 CC diluent containing one or both of an agonist of toll-like receptor 4 and
 CC receptor 9 (TLR-4 and TLR-9), the immunogenic particles comprising Hbc
 CC chimeric protein molecules, and maintaining the patient for a sufficient
 CC time to induce T cells activated against Hbc. The immunogenic epitopes
 CC may be B cell or T cell epitopes. The chimeric vaccine is useful for
 CC treating a patient chronically infected with hepatitis B virus. The
 CC present sequence is a B cell epitope suitable for inclusion in the
 CC chimeric protein of the invention.

Query Match	100.0%	Score 162	DB 8	Length 33
Best Local Similarity	100.0%	Pred. No. 6.2e-18		
Matches 30	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	DAEFRHDSGYEVHHOKLVFPAEDVGSNTGCA	30	
ob	1	DAEFRHDSGYEVHHOKLVFPAEDVGSNTGCA	30	

CC	RESULT 15
CC	AAW47228
CC	AAW47228 standard; peptide; 35 AA.
CC	AAW47228;
CC	22-MAY-1998 (first entry)
CC	Beta-amyloid peptide residues 1-35.
CC	Screening assay; beta-amyloid peptide; treatment; amyloidosis disease;
CC	Alzheimer's disease.
CC	Homo sapiens.
CC	US5721106-A.
CC	24-FEB-1998.
CC	12-SEP-1994; 94US-00304585.
CC	13-AUG-1991; 91US-00744767.
CC	(MINU) UNIV MINNESOTA.
CC	(HARD) HARVARD COLLEGE.
CC	Mantyh PW, Maggio JE;
CC	WPI; 1998-168404/15.
CC	New in vitro screening assay for Alzheimer's disease drugs - comprises
CC	assessing binding of labelled beta-amyloid peptide to silk sample.
CC	Claim 8; Col 31-32; 36pp; English.

CC sample with labeled BAP, optionally in the presence of a test agent,
CC detecting the amount of label bound to the silk and assessing the effect
CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP
CC to silk are potentially useful for treating amyloidosis diseases,
CC especially Alzheimer's disease

Query Match	100.0%	Score 162;	DB 2;	length 35;
Best Local Similarity	100.0%;	Pred. No. 6,7e-18;		
Matches	30;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKG	30	
Db	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKG	30	

RESULT 16
AAE35430
ID AAE35430 standard; peptide; 35 AA

AC	AAE35430;
XX	
DT	17-JUN-2003 (first entry)

DE Abeta peptide #1.

KM All-D-amyloid-beta peptide, Alzheimer's disease, rheumatoid arthritis;
 KM cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KM psoriasis; Reiter's syndrome; Adult Still's disease; Behcet's syndrome;
 KM Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontopic;
 KM chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KM Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KM ulcer; antiinflammatory; cytostatic; urothelial; therapy.

Unidentified.

	Key	Location/Qualifiers
FH	Misc-difference	1. .35
FT		/note= "D-form resi
FT		

PN WO200296937-A2.

05-DEC-2002.

29-MAY-2002; 2002WO-CA000763.

29-MAY-2001; 2001US-00867847.

PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;

WPI; 2003-201269/19.

Prevention and/or treatment of an amyloid-related disease e.g. Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

PS Claim 1; Page 58; 44pp; English.

The invention relates to a method for prevention and/or treatment of an amyloid-related disease which comprises administration of an all-D-amyloid-beta peptide. The method is used for prevention and/or treating Alzheimer's and other amyloid related disease e.g. cerebral amyloid angiopathy; for altering serum levels of amyloid-beta in a mammal and for the clearance of soluble amyloid-beta or fibril amyloid-beta from the mammal; and reducing or inhibiting the formation of plaques. It is also used for treating AA (reactive) amyloid diseases including inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy, Reiter's syndrome, Adult Still's disease, Behcet's syndrome and Crohn's disease. AA deposits are also produced as a result of chronic microbial infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus

CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 CC
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 162; DB 6; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAERFHDGSEVHHQKLVFPAEDVGSNKG 30
 1 DAERFHDGSEVHHQKLVFPAEDVGSNKG 30
 DB
 RESULT 17
 ADQ37254
 ID ADQ37254 standard; peptide; 35 AA.
 AC ADQ37254;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antihypertoid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 KW
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..35
 PT /note= "D-form residues"
 XX
 PN WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 PD 24-DEC-2003; 2003WO-CA002021.
 XX
 PF 24-DEC-2002; 2002US-0436379P.
 XX
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 PA (NEUR-) NEUROCHEM INT LTD.
 XX
 PI Gervais F, Bellini F;
 XX
 DR WPI; 2004-543342/52.
 XX
 PT Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 67; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)

CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotic; neuroprotective; cerebroprotective; haemostatic;
 CC ophthalmological; antihypertoid; vasotropic; cardiovascular; tranquilliser;
 CC uteropathic; anticonvulsant; anti-HIV; antiparkinsonian; muscular;
 CC neuroleptic; cardiant; antidepressant; endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, amnesia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 162; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAERFHDGSEVHHQKLVFPAEDVGSNKG 30
 1 DAERFHDGSEVHHQKLVFPAEDVGSNKG 30
 DB
 RESULT 18
 AAW81471
 ID AAW81471 standard; peptide; 36 AA.
 XX
 AC AAW81471;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Synthetic amyloid beta (Abeta) peptide 6 (residues 1-36).
 XX
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KW research; neurotoxicity; free-radical; glutamine synthetase.
 XX
 OS Synthetic.
 XX
 PN US5840838-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 29-FEB-1996; 96US-00609090.
 XX
 PR 29-FEB-1996; 96US-00609090.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
 DB 7 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 36

RESULT 21

ABR42779 ID ABR42779 standard; protein; 36 AA.

AC ABR42779;

DT 08-SEP-2003 (first entry)

DE Amyloid beta-derived immunogenic polypeptide.

KW Amyloid beta; amyloidosis; Alzheimer's disease; neurotropic; neuroprotective; immunogen; vaccine; human; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

PN WO2003045128-A2.

PD 05-JUN-2003.

PF 21-NOV-2002; 2002WO-US037634.

PR 21-NOV-2001; 2001US-0331801P.

PA (UYNV) UNIV NEW YORK STATE.

PI Frangione B, Wisniewski T, Sigurdsson EM;

DR WPI; 2003-505145/47.

PT New synthetic immunogenic but non-deposit forming peptides, useful for inducing an immune response to prions, amyloids, amylin or amylin fibrils, particularly for treating e.g. Alzheimer's, scrapie or Creutzfeldt-Jacob disease.

PS Example 2; Page 217; 265pp; English.

CC The present sequence is that of a polypeptide, denoted Abeta1-30-K6, comprising amino acid residues 1-30 of amyloid beta(1-42) protein (see also ABR42769) with a C-terminal poly-Lys region. The novel polypeptide was shown to be slightly fibrillogenic in vitro but was non-toxic in human neuronal culture. It is an example of amyloid beta homologous polypeptides of the invention that can be used to induce an immune response to amyloid beta peptides for use in reducing amyloidosis. The use of non-fibrillar/non-toxic amyloid beta polypeptides is a safer vaccination approach for humans

SO Sequence 36 AA;

Query Match 100.0%; Score 162; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 6.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
 DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30

RESULT 22

ABR42774 ID ABR42774 standard; protein; 36 AA.

AC ABR42774;

DT 08-SEP-2003 (first entry)

DE Amyloid beta-derived immunogenic polypeptide.

KW Amyloid beta; amyloidosis; Alzheimer's disease; neurotropic; neuroprotective; immunogen; vaccine; human; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

FT Key location/Qualifiers

FT Modified-site 36 /note="C-terminal amide"

PN WO2003045128-A2.

PD 05-JUN-2003.

PF 21-NOV-2002; 2002WO-US037634.

PR 21-NOV-2001; 2001US-0331801P.

PA (UYNV) UNIV NEW YORK STATE.

PI Frangione B, Wisniewski T, Sigurdsson EM;

DR WPI; 2003-505145/47.

PT New synthetic immunogenic but non-deposit forming peptides, useful for inducing an immune response to prions, amyloids, amylin or amylin fibrils, particularly for treating e.g. Alzheimer's, scrapie or Creutzfeldt-Jacob disease.

PS Example 1; Page 214; 265pp; English.

CC The present sequence is that of a novel immunogenic but non-deposit forming polypeptide derived from amino acid residues 1-30 of amyloid beta(1-42) protein (see also ABR42769). The novel polypeptide, denoted K6Abeta1-30-NH2, maintains the 2 major immunogenic sites of amyloid beta peptides, and is antedated at the C-terminus to further preserve antigenicity. Immunization of transgenic APP mice (Tg2576) for 7 months with this non-amyloidogenic non-toxic amyloid beta homologous peptide reduced cortical and hippocampal brain amyloid burden by 89% and 81%, respectively, and brain levels of soluble amyloid beta(1-42) were reduced by 57%. K6Abeta1-30-NH2 is an example of amyloid beta homologous polypeptides of the invention that can be used to induce an immune response to amyloid beta peptides for use in reducing amyloidosis. The use of non-fibrillar/non-toxic amyloid beta polypeptides is a safer vaccination approach for humans

SO Sequence 36 AA;

Query Match 100.0%; Score 162; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 6.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
 DB 7 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 36

RESULT 23

ADP73823 ID ADP73823 standard; peptide; 36 AA.

AC ADP73823;

DT 09-SEP-2004 (first entry)

DE Loop insertion vector plasmid verification primer peptide, SEQ ID 436.

KW transgenic animal; Hepatitis B virus nucleocapsid core protein; Hbc; enhanced stability; hepatotropic; viraemic; immunology; protein engineering; immunogen; vaccine; Hepatitis B infection.

OS Unidentified.
XX WO2004053091-A2.
XX
XX 24-JUN-2004.
XX
XX 10-DEC-2003; 2003WO-US039164.
XX
XX 10-DEC-2002; 2002US-0432123P.
XX
XX (APOV-) APOVIA INC.
XX
XX Lyons K, Birkett AJ, Haron JA;
XX WPI; 2004-468859/44.
XX
XX New recombinant chimer hepatitis B core (HBC) protein molecules useful in
PT the fields of immunology and protein engineering, in particular as an
PT immunogen in a vaccine for Hepatitis B infections.
XX
XX Example 1; SEQ ID NO 436; 338bp; English.
XX
XX The invention relates to a novel recombinant chimeric Hepatitis B virus
CC nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues
CC in length. The chimeric protein is engineered for both enhanced stability
CC of self-assembled particles and the substantial absence of nucleic acid
CC binding by the particles. The invention further comprises: a recombinant
CC HBC protein chimeric molecule that has a length of 135-365 amino acid
CC residues and contains four peptide-linked amino acid residue sequence
CC domains from the N-terminus that are denominated Domains I, II, III and
CC IV. The invention also provides nucleic acids, polypeptides, host cells,
CC vectors and transgenic animals used in the methods of the invention. The
CC chimeric compositions of the invention have hepatotropic and virulent
CC activities. The methods and compositions of the present invention are
CC useful in the fields of immunology and protein engineering, in particular
CC for using a chimeric hepatitis B virus nucleocapsid protein as an
CC immunogen in a vaccine for Hepatitis B infections. This sequence
CC represents a Hepatitis B virus nucleocapsid (core) protein related
CC polypeptide of the invention.
XX
XX Sequence 36 AA;
SQ
Query Match 100.0%; Score 162; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHMQKLVFPFADVGSNKG 30
DB 3 DAEFRHDSGYEVHMQKLVFPFADVGSNKG 32
RESULT 24
AAE0362
ID AAE0362 standard; peptide; 38 AA.
XX
XX AAR60362;
AC
XX 25-MAR-2003 (revised)
DT 15-MAR-1995 (first entry)
XX
XX Beta-amyloid (1-38).
DE
XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis.
XX
XX Homo sapiens.
OS
XX WO9411797-A1.
PN
XX 04-AUG-1994.
PD
XX 24-JAN-1994; 94WO-JP000089.
PF
XX

PR 25-JAN-1993; 93JP-00010132.
PR 02-FEB-1993; 93JP-00019035.
PR 16-NOV-1993; 93JP-00286985.
PR 28-DEC-1993; 93JP-00334773.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Suzuki N, Odaka A, Kitada C;
XX WPI; 1994-264110/32.
XX
XX Antibodies recognising specific parts of beta-amyloid - can be used for
PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
PT disease.
XX
XX Disclosure; Page 81; 116pp; Japanese.
XX
XX Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
CC the C-terminal portion. The antibodies are useful for assaying beta-
CC amyloid and its derivatives for diagnosis of Alzheimer's disease.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 162; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHMQKLVFPFADVGSNKG 30
DB 1 DAEFRHDSGYEVHMQKLVFPFADVGSNKG 30
RESULT 25
AAW92722
ID AAW92722 standard; peptide; 38 AA.
XX
XX AAW92722;
AC
XX 20-MAR-2003 (revised)
DT 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #68.
DE
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX US5876948-A.
FN
XX 02-MAR-1999.
PD
XX 29-JUL-1991; 91US-00737371.
PF
XX 27-JUL-1990; 90US-00559173.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
PI
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
XX
XX Claim 1b; Col 39-40; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiotachy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
 CC field.)
 CC

SO Sequence 38 AA;

Query Match 100.0%; Score 162; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30

RESULT 26

AAB91826
 ID AAB91826 standard; peptide; 38 AA.

XX AAB91826;

DT 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:1002.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 522; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC

SO Sequence 38 AA;

Query Match 100.0%; Score 162; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30

RESULT 27

AAB91799
 ID AAB91799 standard; peptide; 38 AA.

XX AAB91799;

DT 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:975.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 513; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

SO Sequence 38 AA;

Query Match 100.0%; Score 162; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 28

ADY81762 standard; peptide; 38 AA.

ADY81762;

02-JUN-2005 (first entry)

Human beta-amyloid residues 1-38.

cerebroprotective; neurotropic; neuroprotective; diagnostic;
 antibody therapy; Alzheimer's disease; degeneration; neurological disease;
 cognitive disorder; beta-amyloid; amyloid protein.

Homo sapiens.

WO2005025616-A1.

24-MAR-2005.

08-SEP-2004; 2004WO-JP013397.

09-SEP-2003; 2003JP-00317443.

(TAKE) TAKEDA PHARM CO LTD.

Shoji M, Asami A, Suzuki N;

WPI; 2005-242286/25.

Preventive and therapeutic agent useful for treating and preventing
 Alzheimer's disease, mild cognitive impairment, or brain amyloid
 angiopathy, comprises antibody capable of reacting with partial peptide
 in C-terminal of beta-amyloid.

Claim 5; SEQ ID NO 1; 44pp; Japanese.

The invention describes a preventive and therapeutic agent (I) of an
 Alzheimer's disease, mild cognitive impairment or brain amyloid
 angiopathy, comprising a monoclonal antibody (AI) reacting specifically
 with a partial peptide in the C terminal of beta-amyloid or its
 derivative(s), where AI does not recognize the partial peptide of beta-
 amyloid comprising a 11 amino acid sequence (SEQ ID No. 8) fully defined
 in the specification. (AI) is useful for manufacturing the preventive
 therapeutic agent (I) which is administered in order to prevent and treat
 Alzheimer's disease, mild cognitive impairment or brain amyloid
 angiopathy. (I) is useful as diagnostic agent for Alzheimer's disease.
 (I) is capable of removing beta-amyloid from a formed senile plaque. (I)
 inhibits aggregation of beta-amyloid in the brain. (I) arrests beta-
 amyloid at the periphery region. (I) does not induce bleeding from the
 cerebral blood vessel. This is the amino acid sequence of human beta-
 amyloid residues 1-38.

Sequence 38 AA;

Query Match 100.0%; Score 162; DB 9; Length 38;

Best Local Similarity 100.0%; Pred. No. 7,4e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 29

AA60363 standard; peptide; 39 AA.

AA60363;

25-MAR-2003 (revised)

15-MAR-1995 (first entry)

Beta-amyloid (1-39).

Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 anti-beta-amyloid antibody; diagnosis.

Homo sapiens.

WO9417197-A1.

04-AUG-1994.

24-JAN-1994; 94WO-JP000089.

25-JAN-1993; 93JP-00010132.

05-FEB-1993; 93JP-00019035.

16-NOV-1993; 93JP-00286985.

28-DEC-1993; 93JP-00334773.

(TAKE) TAKEDA CHEM IND LTD.

Suzuki N, Odaka A, Kitada C;

WPI; 1994-264110/32.

Antibodies recognising specific parts of beta-amyloid - can be used for
 diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
 disease.

Disclosure; Page 81; 116pp; Japanese.

Antibodies which recognise specific subfragments of the beta-amyloid
 protein are claimed. Specifically, the antibodies (which are pref.
 monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
 the C-terminal portion. The antibodies are useful for assaying beta-
 amyloid and its derivatives for diagnosis of Alzheimer's disease.
 (Updated on 25-MAR-2003 to correct FN field.)

Sequence 39 AA;

Query Match 100.0%; Score 162; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 7,6e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 30

AAW81472 standard; peptide; 39 AA.

AAW81472;

28-JAN-1999 (first entry)

Synthetic amyloid beta (Abeta) peptide 7 (residues 1-39).

Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 research; neurotoxicity; free-radical; glutamine synthetase.

Synthetic.

PN US5840838-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 29-FEB-1996; 96US-00609090.
 XX
 PR 29-FEB-1996; 96US-00609090.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Akenov M, Carney JM, Hensley K, Butterfield DA;
 XX
 DR WPI; 1999-034120/03.
 XX
 PT Process for treating synthetic amyloid beta peptides - by organic solvent
 PT treatment, useful for studying neurotoxicity.
 XX
 PS Claim 5; Col 11-12; 14pp; English.
 XX
 CC Sequences AAM81466 to AAM81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic Abeta
 CC peptide that comprises dissolving the peptide in a deoxygenated solvent
 CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulfoxide, morpholinopropane sulphonc acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative
 CC deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful
 CC as research tools for studying neurotoxicity resulting from Abeta peptide
 CC -enhanced free-radical production. The treatment increases the activity
 CC of the synthetic Abeta peptides in tests to determine free-radical
 CC generating capacity and glutamine synthetase inactivation
 XX
 SQ Sequence 39 AA;

Query Match 100.0%; Score 162; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 7.6e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 30
 |||||
 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 30

RESULT 31

AAV25134
 ID AAY25134 standard; peptide; 39 AA.

XX
 AC AAY25134;

DT 26-AUG-1999 (first entry)

DE Human amyloid beta-A4 peptide 1.

KM Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
 KW therapeutic drug; brain; Alzheimer's disease.

OS Homo sapiens.

PN US5919631-A.

PD 06-JUL-1999.

PF 17-JUL-1996; 96US-00682245.

PR 17-JUL-1996; 96US-00682245.

PA (HMRI) HOECHST MARION ROUSSEL INC.

PI Sahaarabudhe SR, Paul JW, Goyal S, Riedel NG;

DR WPI; 1999-403957/34.

PT Determination of degree of aggregation of a peptide, useful for

PT identifying therapeutic drugs for treating Alzheimer's disease.

PS Disclosure; Col 5-6; 8pp; English.

CC This invention describes a novel method for the determination of the
 CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
 CC Determination comprises: (a) incubating a sample of unaggregated (I) with
 CC Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated
 CC (I); (b) measuring the amount of (II) bound to (I) to obtain a value (i);
 CC (c) repeating steps (a) and (b) with a second sample at a different time
 CC to obtain a second value (ii); and (d) determining the difference between
 CC (i) and (ii) which is inversely related to the degree of aggregation of
 CC (I). This method may be applied to a screen for compounds that inhibit
 CC aggregation of (I). These inhibitors may be used as therapeutic drugs to
 CC inhibit the formation of these aggregates in the brains of patients
 CC suffering from Alzheimer's disease
 XX
 SQ Sequence 39 AA;

Query Match 100.0%; Score 162; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 7.6e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 30
 |||||
 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 30

RESULT 32

ABU08509
 ID ABU08509 standard; peptide; 39 AA.

XX
 AC ABU08509;

DT 22-MAY-2003 (first entry)

DE Human amyloid beta peptide (1-39).

KM Human; amyloid beta peptide (1-39); Alzheimer's disease; antigen; Abeta.

OS Homo sapiens.

PN US2002182660-A1.

PD 05-DEC-2002.

PF 18-JAN-2002; 2002US-00051496.

PR 18-FEB-2000; 2000US-0183407P.

PR 16-FEB-2001; 2001US-00784854.

PA (FONG/) FONG K L.

PI Fong KL;

DR WPI; 2003-328616/31.

PT Enabling measurement of full length beta-amyloid peptide level for
 PT tracking progression of Alzheimer's disease, comprises capturing and
 PT binding terminus of beta-amyloid peptide with antibodies.

PS Disclosure; Fig 1e; 11pp; English.

CC The invention relates to a measurement of the full length beta-amyloid
 CC (Abeta) peptide level of a specific Abeta peptide in a sample containing
 CC multiple types of Abeta peptide, by capturing and binding one terminus of
 CC the types of Abeta peptides with a first antibody. The specific Abeta
 CC peptide is captured and bound at an opposite non-overlapping terminus
 CC with a second peptide. The invention is used for measuring full length
 CC Abeta peptide level useful for tracking the progression of Alzheimer's
 CC disease. The new method uses one specific antibody that recognises the N-
 CC terminus of all the Abeta peptides and a panel of detection antibodies
 CC that distinguish each Abeta peptide (Abeta 1-43, 1-42, 1-41, 1-40 and 1-

CC 39) by their sequence difference at the C-terminus. This use of N and C-terminus specific antibodies allows simultaneous quantification of several Abeta peptides in a single assay. The present sequence is that of Abeta (1-39), used to raise the N and C-terminal antibodies of the invention

XX Sequence 39 AA;
SQ

Query Match 100.0%; Score 162; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.6e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 33
ABP96148 ID ABP96148 standard; peptide; 39 AA.
XX
AC ABP96148;
XX
DT 12-MAY-2003 (first entry)
XX
DE Human Abeta39 amino acid sequence SEQ ID NO:5.
XX
XX Human; Abeta39; amyloid toxicity inhibition; amyloid; integrin subunit; integrin; laminin; neurotrophic; neuroprotective; antidiabetic; antiparkinsonian; gene therapy; amyloidogenic protein; prion infection; amyloidogenic protein toxicity inhibition; amyloidogenic disease; Alzheimer's disease; type II diabetes; Parkinson's disease; amyloidosis; Down's syndrome.
XX
OS Homo sapiens.
XX
PN WO2003006893-A2.
XX
PD 23-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-US019803.
XX
PR 09-JUL-2001; 2001US-0304315P.
XX
PR 17-DEC-2001; 2001US-0341772P.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Penner IG, Wright S, Yednock T, Rydel R;
XX
DR WPI; 2003-221770/21.
XX
PT Inhibiting amyloid toxicity or the formation of an amyloid deposit, comprises administering an agent that binds to an integrin, integrin subunit, or laminin.
XX
PS Disclosure; Page 85-86; 86pp; English.
XX
XX The present invention describes a method for inhibiting amyloid toxicity or the formation of an amyloid deposit. The method comprises administering a dosage of one or more agent(s) that bind(s) to a molecule selected from an integrin subunit such as alpha2, alpha, alpha6 or beta1, an integrin such as alphabeta1, alphabeta1 or alphabeta1, and laminin, under conditions such that the agent(s) inhibit amyloid toxicity or the formation of an amyloid deposit. Amyloids have neurotrophic, neuroprotective, antidiabetic and antiparkinsonian activities, and can be used in gene therapy. The method is useful for inhibiting amyloidogenic protein toxicity, inhibiting the formation of an amyloidogenic protein deposit and/or treating amyloidogenic diseases, such as Alzheimer's disease, type II diabetes, Parkinson's disease, a disease caused all or in part by prion infection, hereditary or systemic amyloidosis, or Down's syndrome. The present sequence represents a human Abeta peptide designated Abeta39, which is given in the exemplification of the present invention

XX Sequence 39 AA;
SQ

Query Match 100.0%; Score 162; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.6e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 34
ADY81763 ID ADY81763 standard; peptide; 39 AA.
XX
AC ADY81763;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human beta-amyloid residues 1-39.
XX
XX Cerebroprotective; neurotrophic; neuroprotective; diagnostic; immunotherapy; Alzheimer's disease; degeneration; neurological disease; cognitive disorder; beta-amyloid; amyloid protein.
XX
OS Homo sapiens.
XX
PN WO2005025616-A1.
XX
PD 24-MAR-2005.
XX
PF 08-SEP-2004; 2004WO-JP013397.
XX
PR 09-SEP-2003; 2003JP-00317443.
XX
PA (TAKE) TAKEDA PHARM CO LTD.
XX
PI Shoji M, Asami A, Suzuki N;
XX
DR WPI; 2005-242286/25.
XX
PT Preventive and therapeutic agent useful for treating and preventing Alzheimer's disease, mild cognitive impairment, or brain amyloid angiopathy, comprises antibody capable of reacting with partial peptide in C-terminal of beta-amyloid.
XX
PS Claim 5; SEQ ID NO 2; 44pp; Japanese.
XX
XX The invention describes a preventive and therapeutic agent (I) of an Alzheimer's disease, mild cognitive impairment or brain amyloid angiopathy, comprising a monoclonal antibody (A1) reacting specifically with a partial peptide in the C terminal of beta-amyloid or its derivative(s), where A1 does not recognize the partial peptide of beta-amyloid comprising a 11 amino acid sequence (SEQ ID No. 8) fully defined in the specification. (A1) is useful for manufacturing the preventive-therapeutic agent (I) which is administered in order to prevent and treat Alzheimer's disease, mild cognitive impairment or brain amyloid angiopathy. (I) is useful as diagnostic agent for Alzheimer's disease. (I) is capable of removing beta-amyloid from a formed senile plaque. (I) inhibits aggregation of beta-amyloid in the brain. (I) arrests beta-amyloid at the periphery region. (I) does not induce bleeding from the cerebral blood vessel. This is the amino acid sequence of human beta-amyloid residues 1-38.
XX
SQ Sequence 39 AA;
XX

Query Match 100.0%; Score 162; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.6e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
|||||

```

Db      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKG 30

RESULT 35
ID      AAR33191
XX      AAR33191 standard; peptide; 40 AA.
AC      AAR33191;
XX
XX      25-MAR-2003 (revised)
DT      01-JUL-1993 (first entry)
XX
XX      Beta-amyloid peptide.
DE
XX      Alzheimer's disease; amyloid deposition; diagnosis; therapy.
XX      Synthetic.
OS
XX      W09304194-A1.
XX      04-MAR-1993.
XX      10-AUG-1992; 92MO-US006700.
XX      13-AUG-1991; 91US-00744767.
XX      (MINU ) UNIV MINNESOTA.
XX      (HARD ) HARVARD COLLEGE.
XX      Maggio JE, Mantyh PW;
XX      WPI; 1993-094020/11.
XX
XX      Detecting Alzheimer's disease using beta-amyloid peptide - includes
PT      quantitating amyloid deposition onto tissue samples, and using screen
PT      agents as therapeutic agents.
XX
XX      Disclosure; Page 34; 51pp; English.
XX
XX      The peptide is an internal fragment of the beta amyloid peptide (BAP)
CC      precursor, which was produced synthetically. The peptide, when labelled,
CC      may be used in in vitro methods for the detection of Alzheimer's disease.
CC      See also AAR33192. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Sequence 40 AA;
SQ

Query Match      100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKG 30
        ||||||||||||||||||||||||||||
        1 DAEFRHDSGYEVHHQKLVFPFADVGSNKG 30
Db

RESULT 36
ID      AAR60364
XX      AAR60364 standard; peptide; 40 AA.
AC      AAR60364;
XX
XX      25-MAR-2003 (revised)
DT      15-MAR-1995 (first entry)
XX
XX      Beta-amyloid (1-40).
DE
XX      Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW      anti-beta-amyloid antibody; diagnosis.
XX
XX      Homo sapiens.
XX      W09417197-A1.
XX

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```

PD 04-AUG-1994.
XX
PF 24-JAN-1994; 94MO-JP000089.
XX
PR 25-JAN-1993; 93JP-00010132.
XX
PR 05-FEB-1993; 93JP-00019035.
PR 16-NOV-1993; 93JP-00286985.
PR 28-DEC-1993; 93JP-00334773.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Suzuki N, Odaka A, Kitada C;
XX WPI; 1994-264110/32.
XX
XX Antibodies recognising specific parts of beta-amyloid - can be used for
PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
PT disease.
XX
XX Disclosure; Page 82; 116pp; Japanese.
PS
XX
XX Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
CC the C-terminal portion. The antibodies are useful for assaying beta-
CC amyloid and its derivatives for diagnosis of Alzheimer's disease.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKG 30
XX
RESULT 37
ADD11651
ID ADD11651 standard; protein; 40 AA.
XX
AC ADD11651;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human beta-amyloid 1-40 (beta1-40) .
XX
KW neurotoxic effect; beta-amyloid peptide; neurotoxicity inhibitor;
KW amyloidogenic amylin; beta-2-microglobulin; amylin; Alzheimer's disease;
KW Down's syndrome; beta-amyloid neurotoxicity assay; human;
KW beta-amyloid 1-40; beta1-40.
XX
XX Homo sapiens.
XX
OS
XX EP646792-A1.
XX
PN
PD 05-APR-1995.
XX
PF 17-AUG-1994; 94EP-00306053.
XX
PR 19-AUG-1993; 93US-00109782.
XX
XX (ELIL ) LILLY & CO ELT.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
XX May PC, Rydel RE;
XX
XX WPI; 1995-132760/18.
XX
XX Assay for effectiveness of agents used in the treatment of Alzheimer's
XX
XX

```

PT disease - by incubating potential inhibitor of neurotoxicity with amylin
XX or beta-2-microglobulin and measuring neurotoxic props. of mixt.
PS Disclosure; SEQ ID NO 2; 14pp; English.
CC The invention describes a method for assaying the effectiveness of agents
CC useful for ameliorating the neurotoxic effects of a condition associated
CC with the accumulation of a beta-amyloid peptide. The method comprises:
CC (a) incubating potential inhibitors of neurotoxicity with an
CC amyloidogenic amylin or beta-2-microglobulin; (b) measuring the
CC neurotoxic properties of each amylin or beta-2-microglobulin/potential
CC inhibitor mixture; and (c) detecting reduction in the neurotoxicity
CC relative to a control. The preferred amyloidogenic amylin is human
CC amylin. The method is especially for assessing the ability of an agent to
CC ameliorate the neurotoxic effects of Alzheimer's disease or Down's
CC syndrome. The method provides a more consistent beta-amyloid
CC neurotoxicity assay and is more sensitive and covers a broader range.
CC This is the amino acid sequence of human beta-amyloid 1-40 (betal-40).
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 38
ID AAM23335 standard; peptide; 40 AA.
XX
AC AAM23335;
XX
DT 12-MAR-1998 (first entry)
XX
DE Amyloid beta peptide 1 used to inhibit damage to cells in Alzheimer's.
XX
KW Amyloid beta peptide; extracellular deposit; Alzheimer's disease;
KW mericr outgrowth; microglial activation; neuronal cell degeneration;
KW receptor for advanced glycosylation end product;
KW amyloid beta peptide fibril.
XX
OS Homo sapiens.
XX
FN WO9726913-A1.
XX
PD 31-JUL-1997.
XX
PF 21-JAN-1997; 97WO-US000857.
XX
PR 26-JAN-1996; 96US-00592070.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Stern D, Schmidt AM, Yan SD;
XX
PI WPI; 1997-393374/36.
XX
PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an agent
PT which inhibits interaction of an amyloid-beta peptide with a receptor for
XX advanced glycosylation end product.
XX
PS Claim 4; Page 10; 91pp; English.
XX
CC Peptides AAM23335-36 are portions of the the amyloid beta peptide, which
CC is the principal component of extracellular deposits in Alzheimer's
CC disease. It has been shown to promote neurite outgrowth, generate
CC reactive oxygen intermediates, induce cellular oxidant stress, lead to
CC neuronal cytotoxicity, and promote microglial activation. The present
CC peptide, which comprises amino acids 1-40 of the amyloid beta peptide, is

CC used in a pharmaceutical composition. This composition comprises an agent
CC capable of inhibiting interaction of an amyloid-beta peptide with a
CC receptor for advanced glycosylation end product and a carrier. A method
CC for inhibiting interaction of amyloid beta peptide with a receptor for
CC advanced glycosylation on the surface of a cell comprises contacting the
CC cell with e.g. present peptide. Depending on the type of cell, inhibiting
CC the interaction between the amyloid beta peptide and the receptor for
CC advanced glycosylation can be used for inhibiting degeneration of a
CC neuronal cell, inhibiting formation of an amyloid beta peptide fibril on
CC a cell, inhibiting aggregation assembly of amyloid beta peptide into a
CC fibril, inhibiting infiltration of a microglial cell into senile plaques,
CC and inhibiting activation of microglial cells by amyloid beta peptide.
CC The methods can be used for treating e.g. diabetes, Alzheimer's Disease,
CC senility, renal failure, hyperlipidemic atherosclerosis, neuronal
CC cytotoxicity, Down's syndrome, dementia associated with head trauma,
CC amyotrophic lateral sclerosis, multiple sclerosis or neuronal
XX degeneration
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 39
ID AAM37507 standard; peptide; 40 AA.
XX
AC AAM37507;
XX
DT 20-APR-1998 (first entry)
XX
DE Amyloid beta protein fragment (1-40) immunogen.
XX
KW Amyloid beta protein; A beta; immunogen; human; Alzheimer's disease;
KW amyloid precursor protein; soluble; APP; monoclonal antibody; diagnosis.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Cleavage-site 16..17
XX
FN EP783104-A1.
XX
PD 09-JUL-1997.
XX
PF 17-DEC-1996; 96EP-00120269.
XX
PR 27-DEC-1995; 95JP-00351296.
XX
PA (ORIX) ORIENTAL YEAST CO LTD.
XX
PI Taniguchi Y, Fujita T, Matuo Y;
XX
PI WPI; 1997-343989/32.
XX
PT Assay for soluble amyloid precursor protein useful to diagnose
PT Alzheimer's disease - uses antibodies against amyloid beta-protein, also
XX new hybridoma producing antibodies.
XX
PS Example 1; Fig 2; 10pp; English.
XX
CC A novel method has been developed of assaying for soluble amyloid
CC precursor protein (sAPP). The method uses an antibody against amyloid
CC beta-protein (A beta; produced from sAPP) or sAPP. The present sequence
CC represents amino acids 1 to 40 of amyloid beta-protein. sAPP can be

CC assayed accurately, and when including a monoclonal antibody recognising
CC the N-terminus of A beta and a monoclonal antibody recognising SAP, the
CC assay can be used to diagnose Alzheimer's disease. Senior plaque observed
CC in the brain of Alzheimer's patients is primarily composed of A beta ,
CC which is generated from SAP. Simple and accurate assay of SAP is
CC possible. The antibody (preferably monoclonal) preferably has an antigen
CC recognition site which is an amino acid sequence common to A beta and
CC SAP, or specific to SAP. The SAP assayed for preferably has part of
CC the A beta sequence at its amino terminus and is preferably solubilised
CC through cleavage of the A beta between positions 16 (lysine) and 17
CC (leucine) from the amino acid terminus. The preferred method comprises
CC immobilising one antibody (especially generated by (2)) on to an
CC insoluble carrier, capturing a substance to be assayed on to this
CC antibody, reacting another, labelling, antibody with the assay substance
CC and detecting the activity of the labelling substance bound to the
CC carrier
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 40
AAM47226
ID AAM47226 standard; peptide; 40 AA.
XX
AC AAM47226;
XX
DT 22-MAY-1998 (first entry)
XX
DB Beta-amyloid peptide residues 1-40.
XX
DE
XX Screening assay; beta-amyloid peptide; treatment; amyloidosis disease;
KM Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5721106-A.
XX
PD 24-FEB-1998.
XX
PF 12-SEP-1994; 94US-00304585.
XX
PR 13-AUG-1991; 91US-00744767.
XX
PA (MINU) UNIV MINNESOTA.
PA (HARD) HARVARD COLLEGE.
XX
PI Mantylh PW, Maggio JB;
XX
DR WPI; 1998-168404/15.
XX
PT New in vitro screening assay for Alzheimer's disease drugs - comprises
PT assessing binding of labelled beta-amyloid peptide to silk sample.
XX
PS Claim 8; Col 29-30; 36pp; English.
XX
CC The present sequence was used in the development of a novel in vitro
CC screening assay for agents capable of affecting the deposition of beta-
CC amyloid peptide (BAP) on tissue. The method comprises contacting a silk
CC sample with labelled BAP, optionally in the presence of a test agent,
CC detecting the amount of label bound to the silk and assessing the effect
CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP
CC to silk are potentially useful for treating amyloidosis diseases,
CC especially Alzheimer's disease
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 41
AA14099
ID AA14099 standard; peptide; 40 AA.
XX
AC AA14099;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human beta-amyloid protein fragment.
XX
DE
XX Beta-amyloid; human; amyloid plaque deposition; Alzheimer's disease;
KM induction; AD; sleep; circadian activity; circadian rhythm disturbance.
XX
OS Homo sapiens.
XX
PN WO921978-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98WO-US022731.
XX
PR 28-OCT-1997; 97US-00959148.
XX
PA (MIRI-) MIRIAM HOSPITAL LIFESPAN PARTNER.
XX
PI Majocha R, Tate BA, Newton JL;
XX
DR WPI; 1999-326700/27.
XX
FT Inducing amyloid plaque deposition in a mammal, used to screen for agents
PT against Alzheimer's disease.
XX
PS Claim 2; Page 30; 43pp; English.
XX
CC This sequence represents a fragment of the human beta-amyloid protein,
CC and can be used in the method of the invention. The method is for
CC inducing amyloid plaque deposition in a mammal by infusing into the brain
CC an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque
CC deposition has been induced are models of human Alzheimer's disease (AD)
CC and are used to screen for agents (A) that inhibit: (a) deposition of
CC amyloid plaque; and (b) AD-associated disruptions to sleep and circadian
CC activity. They may also be used to study the etiology of AD. Compared
CC with known methods for inducing plaque deposition, this process causes
CC less mechanical damage; the vehicle used is less neurotoxic and at basic
CC pH (I) is soluble enough for delivery by continuous infusion with
CC effective delivery to brain tissue. The control peptide causes few, if
CC any, plaques and does not stimulate an immune response. Most (I)-treated
CC animals develop AD-type pathology (contrast transgenic models of the
CC disease), including sleep and circadian rhythm disturbances
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 42
AA139804

```

ID AAY39804 standard; peptide: 40 AA.
XX
AC AAY39804;
XX
DT 29-NOV-1999 (first entry)
XX
DE Beta-amyloid protein, Beta/A4 amyloid (1-40).
XX
KM Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
KM long-standing inflammation; malignancy; Familial Mediterranean fever;
KM multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
KM carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
KM endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
KM Creutzfeldt-Jakob disease; Gerstmann Strausler Syndrome;
KM subacute spongiform encephalopathy; therapy.
XX
OS Homo sapiens.
XX
PN US5958883-A.
XX
PD 28-SEP-1999.
XX
PF 05-JUN-1995; 95US-00461216.
XX
PR 23-SEP-1992; 92US-00950417.
XX
PR 23-OCT-1992; 92US-00969734.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Snow AD;
XX
DR WPI; 1999-561062/47.
XX
PT Peptides of 6-8 amino acids useful for treating or preventing
XX amyloidosis.
XX
PS Disclosure; Col 67-68; 83pp; English.
XX
CC This sequence represents a fragment of the beta-amyloid protein. The
CC invention relates to a method for treating or preventing a form of
CC amyloidosis, including Alzheimer's disease using this sequence. The
CC composition may be useful for treating or preventing the amyloidosis
CC associated with long-standing inflammation or various forms of malignancy
CC (including B-cell type malignancies), Familial Mediterranean fever,
CC multiple myeloma, plasma cell dyscrasia, long-term haemodialysis, carpal
CC tunnel syndrome, joint swelling, multiple spontaneous fractures, carpal
CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
CC Creutzfeldt-Jakob disease, Gerstmann Strausler Syndrome, kuru, scrapie
CC and other subacute spongiform encephalopathies
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVNHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVNHQKLVFFAEDVGSNKG 30
XX
RESULT 43
AAM99584
ID AAM99584 standard; peptide: 40 AA.
XX
AC AAM99584;
XX
DT 22-JUN-1999 (first entry)
XX
DE Wild type aggregating amyloid-beta peptide.
XX
XX Aggregation; amyloid-beta peptide; fluorescent group; detection;

```

```

KV diagnosis; Alzheimer's disease.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN K09908695-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WC-US016809.
XX
PR 14-AUG-1997; 97US-0055660P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Glabe C, Garzon-Rodriguez W;
XX
DR WPI; 1999-190112/16.
XX
PT New fluorescent labeled amyloid A-beta peptides.
XX
PS Example 1; Page 21; 50pp; English.
XX
CC This sequence corresponds to an aggregating amyloid-beta peptide which
CC can be covalently labelled with a fluorescent group. The detection or
CC monitoring of an amyloid aggregate in a sample can be used to diagnose or
CC detect a predisposition to Alzheimer's disease. The screening assays can
CC be used to identify compounds for the treatment or amelioration of
CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
CC amyloid-beta peptide are also useful for exploring other aspects of the
CC amyloid structure
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVNHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVNHQKLVFFAEDVGSNKG 30
XX
RESULT 44
AAM81473
ID AAM81473 standard; peptide: 40 AA.
XX
AC AAM81473;
XX
DT 28-JAN-1999 (first entry)
XX
DE Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
XX
KM Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KM research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS Synthetic.
XX
PN US5840838-A.
XX
PD 24-NOV-1998.
XX
PF 29-FEB-1996; 96US-00609090.
XX
PR 29-FEB-1996; 96US-00609090.
XX
PA (KENT ) UNIV KENTUCKY RES FOUND.
XX
PI Akeonov M, Carney JM, Hensley K, Butterfield DA;
XX
DR WPI; 1999-034120/03.
XX
PT Process for treating synthetic amyloid beta peptides - by organic solvent

```


PT treatment, useful for studying neurotoxicity.

XX Claim 5; Col 11-12; 14pp; English.

XX

CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetone to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation

CC

XX Sequence 40 AA;

SO

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPFHDSGYEVHMQKLVFPAEDVGSNKGA 30
|||||
DB 1 DAEPFHDSGYEVHMQKLVFPAEDVGSNKGA 30

RESULT 45
AAV39339
ID AAV39339 standard; protein; 40 AA.
XX
XX AAV39339;
XX
XX 01-DEC-1999 (first entry)
XX
XX Beta-amyloid protein.
XX
XX Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque;
XX
XX cerebral blood vessel; sulphated macromolecule; Kuru;
XX
XX congoophilic maltese-cross spherical amyloid plaque;
XX
XX Creutzfeldt-Jacob disease; Gerstmann-Strausler syndrome.
XX
XX Homo sapiens.
XX
XX MO9945947-A1.
XX
XX 16-SEP-1999.
XX
XX 12-MAR-1999; 99WO-US005438.
XX
XX 13-MAR-1998; 98US-0077924P.
XX
XX (UNIV) UNIV WASHINGTON.
XX
XX Castillo G, Snow AD;
XX
XX WPI; 1999-571686/48.
XX
XX Formation of amyloid plaques using amyloid protein and sulfated
PT macromolecules, for, e.g. identification of agents for treating
PT Alzheimer's disease.
XX
XX Claim 3; Page 87; 89pp; English.

CC This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's
CC disease is characterized by the accumulation of a 39-43 amino acid
CC peptide termed the beta-amyloid peptide in the form of extracellular
CC amyloid plaques and as amyloid in the walls of cerebral blood vessels.
CC The invention relates to methods for the formation of congoophilic maltese
CC -cross spherical amyloid plaques, which are characteristic of Alzheimer's
CC disease. The amyloid plaques are formed by co-incubation of this beta-
CC amyloid protein with sulphated macromolecules. The methods can be used to

CC study the formation of amyloid plaques and to identify anti-plaque
CC therapeutics. They can be used for diseases such as Alzheimer's disease,
CC Creutzfeldt-Jacob disease, Gerstmann-Strausler syndrome and Kuru

XX

XX Sequence 40 AA;

SO

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPFHDSGYEVHMQKLVFPAEDVGSNKGA 30
|||||
DB 1 DAEPFHDSGYEVHMQKLVFPAEDVGSNKGA 30

RESULT 46
AAV25135
ID AAV25135 standard; peptide; 40 AA.
XX
XX AAV25135;
XX
XX 26-AUG-1999 (first entry)
XX
XX Human amyloid beta-A4 peptide 2.
XX
XX Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
XX
XX therapeutic drug; brain; Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX US5919631-A.
XX
XX 06-JUL-1999.
XX
XX 17-JUL-1996; 96US-00682245.
XX
XX 17-JUL-1996; 96US-00682245.
XX
XX 17-JUL-1996; 96US-00682245.
XX
XX (HMRI) HOECHST MARION ROUSSEL INC.
XX
XX Sahaarabudhe SR, Paul JW, Goyal S, Riedel NG;
XX
XX WPI; 1999-403957/34.
XX
XX Determination of degree of aggregation of a peptide, useful for
PT identifying therapeutic drugs for treating Alzheimer's disease.
PT
XX
XX Disclosure; Col 5-6; 8pp; English.
XX
XX This invention describes a novel method for the determination of the
CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
CC Determination comprises: (a) incubating a sample of unaggregated (I) with
CC Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated
CC (I); (b) measuring the amount of (II) bound to (I) to obtain a value (1);
CC (c) repeating steps (a) and (b) with a second sample at a different time
CC to obtain a second value (1i); and (d) determining the difference between
CC (1) and (1i) which is inversely related to the degree of aggregation of
CC (I). This method may be applied to a screen for compounds that inhibit
CC aggregation of (I). These inhibitors may be used as therapeutic drugs to
CC inhibit the formation of these aggregates in the brains of patients
CC suffering from Alzheimer's disease

XX

XX Sequence 40 AA;

SO

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPFHDSGYEVHMQKLVFPAEDVGSNKGA 30
|||||
DB 1 DAEPFHDSGYEVHMQKLVFPAEDVGSNKGA 30

RESULT 47
AAW92723
ID AAW92723 standard; peptide; 40 AA.
XX
AC AAW92723;
XX
DT 20-MAR-2003 (revised)
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #69.
XX
KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 29-JUL-1991; 91US-00737371.
XX
PR 27-JUL-1990; 90US-00559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
XX
PS Claim 1b; Col 41-42; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
XX
RESULT 48
AAB84426
ID AAB84426 standard; peptide; 40 AA.
XX
AC AAB84426;
XX
DT 22-AUG-2001 (first entry)
XX
DE Partial sequence of a human beta-amyloid precursor protein.
XX
KM Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
KM vaccine.
XX
OS Homo sapiens.
XX

PN WO200142306-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US033203.
XX
PR 08-DEC-1999; 99US-0169687P.
XX
PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
XX
PI Chain B;
XX
DR WPI; 2001-381648/40.
XX
PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
PT epitope from naturally occurring internal peptide cleavage product (such
PT as beta amyloid peptide) of a precursor protein, joined to T cell
PT epitope.
XX
PS Claim 3; Page 41; 47pp; English.
XX
CC The present sequence represents a partial sequence of a human beta-
CC amyloid precursor protein (APP). The peptide is used to create chimeric
CC peptides of the invention. The chimeric peptides contain a N- or C-
CC terminal end-specific B cell epitope from a naturally occurring internal
CC peptide cleavage product of a precursor or mature protein, as a free N-
CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
CC reduce or prevent the accumulation of amyloid beta peptide in the
CC extracellular space, interstitial fluid and cerebrospinal fluid of the
CC brain, and aggregation into senile amyloid deposits or plaques. They also
CC block the interaction of amyloid beta peptides with other molecules that
CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
CC useful for immunizing humans against the free N- or C-terminus of an
CC internal self peptide cleavage product (e.g. APP peptide) derived from a
CC precursor protein or a mature protein. The internal peptide cleavage
CC product is the self molecule of the mammal
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
XX
RESULT 49
AAB91813
ID AAB91813 standard; peptide; 40 AA.
XX
AC AAB91813;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:989.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy1; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
XX

PR	10-SEP-1999;	99US-0153406P.
PR	15-OCT-1999;	99US-0159783P.
PA	(CONJ-) CONJUCHEM INC.	
XX	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;	
PI	WPI; 2001-112059/12.	
DR		
PT	Modifying and attaching therapeutic peptides to albumin prevents	
PT	peptidase degradation, useful for increasing length of in vivo activity.	
XX		
PS	Disclosure; Page 518; 733pp; English.	
XX		
CC	The present invention describes a modified therapeutic peptide (I)	
CC	comprising a therapeutically active amino acid region (III) and a	
CC	reactive group (II) (e.g. succinimidyl and maleimido groups) attached to	
CC	a less therapeutically active amino acid region (IV), which covalently	
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a	
CC	peptide stabilised therapeutic peptide composed of 3-50 amino acids.	
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth	
CC	factors and neurotransmitters, to protect them from peptidase activity in	
CC	vivo for the treatment of various disorders. Endogenous therapeutic	
CC	peptides are not suitable as drug candidates as they require frequent	
CC	administration due to rapid degradation by peptidases in the body.	
CC	Modifying and attaching therapeutic peptides to albumin prevents or	
CC	reduces the action of peptidases to increase length of activity (half	
CC	life) and specifically as bonding to large molecules decreases	
CC	intracellular uptake and interference with physiological processes.	
CC	AAS90829 to AAB92441 represent peptides which can be used in the	
CC	exemplification of the present invention	
XX		
SQ	Sequence 40 AA;	
	Query Match	100.0%; Score 162; DB 4; Length 40;
	Best Local Similarity	100.0%; Pred. No. 7, 9e-18;
	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dy	1 DAEFRHDSGYEVHHQKLVFPADVGSNNKA 30 1 DAEFRHDSGYEVHHQKLVFPADVGSNNKA 30	
Db	1 DAEFRHDSGYEVHHQKLVFPADVGSNNKA 30	
RESULT 50		
ID	AAB91780	
XX	AAB91780 standard; peptide; 40 AA.	
AC	AAB91780;	
XX		
DT	22-JUN-2001 (first entry)	
XX		
DE	Amyloid beta-protein fragment peptide SEQ ID NO:956.	
XX		
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;	
KW	blood component; modification; succinimidyl; maleimido group; amino;	
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO200069900-A2.	
XX		
PD	23-NOV-2000.	
XX		
PE	17-MAY-2000; 2000WO-US013576.	
XX		
PR	17-MAY-1999; 99US-0134406P.	
PR	10-SEP-1999; 99US-0153406P.	
PR	15-OCT-1999; 99US-0159783P.	
XX		
PA	(CONJ-) CONJUCHEM INC.	
XX	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;	

XX	WP1: 2001-112059/12.
XX	
DR	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity.
XX	
PS	Disclosure; Page 506; 733pp; English.
XX	
CC	The present invention describes a modified therapeutic peptide (I)
CC	comprising a therapeutically active amino acid region (III) and a
CC	reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity in
CC	vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specifically as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AA990829 to AA992441 represent peptides which can be used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 40 AA;
Query Match	100.0%; Score 162; DB 4; Length 40;
Best Local Similarity	100.0%; Pred. No. 7, 9e-18;
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 DAEFRHDSGYEVHHQKLVFPADYGSNKGCA 30
Db	1 DAEFRHDSGYEVHHQKLVFPADYGSNKGCA 30
RESULT 51	
AAB91829	
ID	AAB91829 standard; peptide; 40 AA.
XX	
AC	AAB91829;
XX	
DT	22-JUN-2001 (first entry)
XX	
DE	Amyloid beta-protein fragment peptide SEQ ID NO:1005.
XX	
KM	Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM	blood component; modification; succinimidy1; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FN	WO200069900-A2.
XX	
PD	23-NOV-2000.
XX	
PE	17-MAY-2000; 2000WO-US013576.
XX	
FR	17-MAY-1999; 99US-0134406P.
FR	10-SEP-1999; 99US-0153406P.
PR	15-OCT-1999; 99US-0159783P.
XX	
PA	(CONJ-) CONJUCHEM INC.
XX	
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX	
DR	WP1: 2001-112059/12.
XX	
PT	Modifying and attaching therapeutic peptides to albumin prevents
XX	peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 523; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimide) and material groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity in

CC vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention

XX

SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 4; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHNRKLVFPAEDVGSNKGA 30

Db 1 DAEFRHDSGYEVHNRKLVFPAEDVGSNKGA 30

RESULT 52

AAB91802

ID AAB91802 standard; peptide; 40 AA.

XX

AC AAB91802;

XX

DT 22-JUN-2001 (first entry)

XX

DE Amyloid beta-protein fragment peptide SEQ ID NO: 978.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimide; malonimide group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

XX

XX WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013576.

XX

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX

XX (CONJ-) CONJUCHEM INC.

XX

PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX

PI WPI; 2001-112059/12.

XX

DR WPI; 2001-112059/12.

XX

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity.

XX

XX Disclosure; Page 514; 733pp; English.

PS

XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimide) and material groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity in

CC vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention

XX

SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 4; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHNRKLVFPAEDVGSNKGA 30

Db 1 DAEFRHDSGYEVHNRKLVFPAEDVGSNKGA 30

RESULT 53

AAB05483

ID AAB05483 standard; peptide; 40 AA.

XX

AC AAB05483;

XX

DT 24-SEP-2001 (first entry)

XX

DE Human peptide antigen comprising beta amyloid (Abeta) 40.

XX

KW Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive;

KW neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;

KW age-related cognitive function loss; senile dementia; Wilson's disease;

KW Parkinson's disease; amyotrophic lateral sclerosis; cerebroprotective;

KW cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;

KW Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;

KW Creutzfeldt-Jakob disease; polyglutamine disease; Huntington's disease;

KW myoclonic dysatropy; neuropsychiatric disorder; seizure disorder; stroke;

KW Gilles de la Tourette's syndrome; nocturnal; chronic seizure disorder;

KW brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;

KW AIDS; dementia; alcoholism; autism; retinal ischaemia; ophthalmological;

KW autonomic function disorder; Freidrich's ataxia; schizophrenia; therapy;

KW vasotropic; neuroprotective; anti-HIV human immunodeficiency virus;

KW anticonvulsant; epilepsy; neuroleptic; immunostimulant.

XX

OS Homo sapiens.

XX

XX WO200152890-A1.

XX

PD 26-JUL-2001.

XX

PF 18-JAN-2001; 2001WO-US001825.

XX

PR 21-JAN-2000; 2000US-00489216.

XX

XX (UYCO-) UNIV CONNECTICUT HEALTH CENT.

XX

PA Srivastava PK;

XX

PI WPI; 2001-451897/48.

XX

DR WPI; 2001-451897/48.

XX

PT Heat shock protein and antigenic molecule complexes, useful for the

PT prevention and treatment of neurodegenerative disorders e.g. senile

PT dementia, Alzheimer's disease and epilepsy.

XX

XX Disclosure; Page 13; 65pp; English.

PS

XX The present invention relates to pharmaceutical compositions comprising

CC complexes of heat shock proteins (hsps) in association with antigenic
 CC molecules for use in treatment and prevention of neurodegenerative
 CC disorders and diseases. The complexes of hsp and antigenic peptides are
 CC used as vaccines for the treatment or prevention of neurodegenerative
 CC disorders e.g. Alzheimer's disease, age-related loss of cognitive
 CC function, senile dementia, Parkinson's disease, amyotrophic lateral
 CC sclerosis, Wilson's disease, cerebral palsy, progressive supranuclear
 CC palsy, Guam disease, Lewy body dementia, prion diseases, spongiform
 CC encephalopathies, Creutzfeldt-Jakob disease, polyglutamine diseases,
 CC Huntington's disease, myotonic dystrophy, Friedreich's ataxia, ataxia,
 CC Gilles de la Tourette's syndrome, seizure disorders, epilepsy, chronic
 CC seizure disorder, stroke, brain trauma, spinal cord trauma, acquired
 CC immunodeficiency syndrome (AIDS) dementia, alcoholism, autism, retinal
 CC ischaemia, glaucoma, autonomic function disorder, hypertension,
 CC neuropsychiatric disorder, schizophrenia or schizoaffective disorder and
 CC for eliciting an immune response. The present sequence is human peptide
 CC antigen comprising beta amyloid (Abeta) 40

SO Sequence 40 AA;
 Query Match 100.0%; Score 162; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFPADVGSNKGA 30
 |||||
 DB 1 DAEFRHDSGYEVHHOKLVFPADVGSNKGA 30

RESULT 54
 AAU99425
 ID AAU99425 standard; peptide; 40 AA.

AC AAU99425;
 XX
 DT 07-OCT-2002 (first entry)

DE Human amyloid beta-peptide (Abeta) fragment (residues 1-40).

XX I-helical conformation; discordant helix; amyloid beta-peptide; I-helix;
 KW cheta-strand structure; amyloidogenic disorder; Abeta; amyloidosis;
 KW Alzheimer's disease; prion disease; scrapie; BSE;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jacob disease; CJD;
 KW fibrillation; aggregation; neurotropic; neuroprotective; human.

XX Homo sapiens.
 XX WO200241002-A2.

PD 23-MAY-2002.

XX 20-NOV-2001; 2001WO-GB005117.

XX 20-NOV-2000; 2000US-0253695P.

PR 06-DEC-2000; 2000US-0251662P.

XX (ALPH-) ALPHABETA AB.

PA (WHIT/) WHITE M P.

XX White MP, Johansson J;

XX MPI, 2002-519389/55.

DR Identifying compounds that stabilize I-helix of discordant helix in
 XX polypeptide, by measuring amount of I-helix in sample containing
 PT discordant helix-containing polypeptide in presence and absence of
 XX compound.

PS Example 4; Page 34; 55pp; English.

XX The present invention relates to a method of identifying a compound that
 CC stabilises an I-helical conformation of a discordant helix in a
 CC polypeptide, particularly amyloid beta-peptide (Abeta). The method

CC comprises providing a test sample comprising a polypeptide that contains
 CC a discordant helix in the form of an I-helix, contacting the test sample
 CC with a test compound and determining the rate of decrease in the amount
 CC of I-helix or the amount of I-helix present in the test sample. The
 CC method is useful for identifying a compound that stabilises an I-helical
 CC conformation of a discordant helix in a polypeptide. Such compounds are
 CC useful for decreasing the rate of formation of cheta-strand structures
 CC between at least two discordant helix-containing polypeptides, and for
 CC treating amyloidogenic disorders such as amyloidosis in Alzheimer's
 CC disease, and prion diseases (e.g. scrapie, bovine spongiform
 CC encephalopathy (BSE), Creutzfeldt-Jacob disease (CJD)). The present
 CC sequence represents human Abeta fragment (amino acid residues 1-40)

SO Sequence 40 AA;
 Query Match 100.0%; Score 162; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFPADVGSNKGA 30
 |||||
 DB 1 DAEFRHDSGYEVHHOKLVFPADVGSNKGA 30

RESULT 55
 AAE22990
 ID AAE22990 standard; peptide; 40 AA.

AC AAE22990;

DT 21-AUG-2002 (first entry)

DE Human amyloid-beta (A-beta) peptide.

XX Human; low-density lipoprotein receptor related protein-1; depression;
 KW Alzheimer's disease; neurodegenerative disorder; Huntington's disease;
 KW Parkinson's disease; multiple sclerosis; Creutzfeldt-Jacob disease;
 KW dementia; LRP-1; confusion; stroke; amyloid-beta peptide; A-beta.

XX Homo sapiens.

XX WO200190758-A2.

PD 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US016561.

XX 23-MAY-2000; 2000US-0206428P.

PR 06-NOV-2000; 2000US-0246268P.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Zlokovic BV;

XX MPI, 2002-083127/11.

DR Method for diagnosing Alzheimer's disease or identifying individual at
 XX risk of developing disease.

XX Example; Page 17; 46pp; English.

XX The invention relates to a method for diagnosing Alzheimer's disease or
 CC identifying an individual at risk of the developing the disease. The
 CC method involves measuring abundance of low-density lipoprotein receptor
 CC related protein-1 (LRP-1), abundance of transcripts thereof, or LRP-1
 CC receptor activity. The method is useful for treating neurodegenerative
 CC disorders such as dementia, depression, confusion, Creutzfeldt-Jacob
 CC disease, Huntington's disease, Parkinson's disease, multiple sclerosis,
 CC loss of motor coordination, stroke and syncope. The present sequence is
 CC human amyloid-beta (A-beta) peptide used in the exemplification of the
 CC invention

XX Sequence 40 AA;

Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 56
AAU11773 standard; protein, 40 AA.
XX AAU11773;
XX 26-MAR-2002 (first entry)
XX Synthetic immunogenic non-amyloidogenic peptide #7.
XX Amyloid beta; non-amyloidogenic peptide; vaccine; immunogen;
KM Alzheimer's disease; amyloid fibril; human.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 31..34 /label= Lys, Asp
FT /note= "Optionally absent"
FT Misc-difference 35..40 /label= Lys, Asp
FT /note= "Optionally absent. When present they form in
FT combination with residues 31-34 a C-terminal polylysine
FT or polyaspartate segment of 4-10 residues in length"

W0200190182-A2.
XX 29-NOV-2001.
XX 22-MAY-2001; 2001WO-US016322.
XX 22-MAY-2000; 2000US-0205578P.
XX (UTNY) UNIV NEW YORK STATE.
XX Frangione B, Wisniewski T, Sigurdson EM;
XX WPI; 2002-106186/14.
XX Novel isolated synthetic immunogenic but non-amyloidogenic peptide
XX homologous to amyloid beta, useful for inducing immune response to
XX amyloid beta peptides and amyloid deposits.
XX Claim 1; Page 66; 69pp; English.
XX The invention relates to an isolated synthetic immunogenic but non-
XX amyloidogenic peptide homologous to amyloid beta. The peptide may be
XX conjugated to polymer molecule. Antibodies raised against the peptides
XX are also included. The peptide is useful for inducing an immune response
XX to amyloid beta peptides and amyloid deposits and therefore treating
XX Alzheimer's disease. The antibody is useful for reducing the formation of
XX amyloid fibrils and deposits. The peptide has a reduced ability to adopt
XX a beta-sheet conformation as an antigenic source, and a much lower risk
XX of leading to any toxic effects in humans. The present sequence is a
XX synthetic immunogenic but non-amyloidogenic peptide of the invention
SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 57
AAU11772 standard; protein, 40 AA.
XX AAU11772;
XX 26-MAR-2002 (first entry)
XX Synthetic immunogenic non-amyloidogenic peptide #6.
XX Amyloid beta; non-amyloidogenic peptide; vaccine; immunogen;
KM Alzheimer's disease; amyloid fibril; human.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 1..6 /label= Lys, Asp
FT /note= "Optionally absent"
FT Misc-difference 7..10 /label= Lys, Asp
FT /note= "Optionally absent or are all Lys or all Asp to
FT form, in combination with residues 1..6, a polylysine or
FT polyaspartate segment of 4-10 residues in length"

W0200190182-A2.
XX 29-NOV-2001.
XX 22-MAY-2001; 2001WO-US016322.
XX 22-MAY-2000; 2000US-0205578P.
XX (UTNY) UNIV NEW YORK STATE.
XX Frangione B, Wisniewski T, Sigurdson EM;
XX WPI; 2002-106186/14.
XX Novel isolated synthetic immunogenic but non-amyloidogenic peptide
XX homologous to amyloid beta, useful for inducing immune response to
XX amyloid beta peptides and amyloid deposits.
XX Claim 1; Page 66; 69pp; English.
XX The invention relates to an isolated synthetic immunogenic but non-
XX amyloidogenic peptide homologous to amyloid beta. The peptide may be
XX conjugated to polymer molecule. Antibodies raised against the peptides
XX are also included. The peptide is useful for inducing an immune response
XX to amyloid beta peptides and amyloid deposits and therefore treating
XX Alzheimer's disease. The antibody is useful for reducing the formation of
XX amyloid fibrils and deposits. The peptide has a reduced ability to adopt
XX a beta-sheet conformation as an antigenic source, and a much lower risk
XX of leading to any toxic effects in humans. The present sequence is a
XX synthetic immunogenic but non-amyloidogenic peptide of the invention
SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 11 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 40

```

RESULT 58
PN AAG68313
ID AAG68313 standard; peptide; 40 AA.
XX
AC AAG68313;
XX
DT 21-FEB-2002 (first entry)
XX
DE Human beta amyloid related amino acid sequence SEQ ID NO:1.
XX
KM Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;
KW amyloid precursor protein; APP.
XX
OS Homo sapiens.
XX
PN WO200182967-A1.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-JP003555.
XX
PR 28-APR-2000; 2000JP-00131037.
XX
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI (SUZU ) SUZUKI T.
XX
PI Suzuki T, Watanabe T, Kawabata S, Hachiya S;
XX
DR WPI; 2002-026209/03.
XX
PT Medicinal compositions for the treatment of dementia and Alzheimer's
XX
PT disease, comprise compounds that suppress beta amyloid production.
XX
PS Example 1; Page 30; 62pp; Japanese.
XX
CC The present invention describes medicinal compositions (1) inhibiting
CC beta-amyloid production comprising an active component a substance that
CC inhibits the activity of cyclin-dependent kinase (CDK). Also described
CC are: (1) a method for screening compounds for their ability to inhibit
CC the production of beta-amyloid by contacting with beta-amyloid producing
CC cells; and (2) screening kits. (1) have neurotropic and neuroprotective
CC activities. (1) suppress the phosphorylation of amyloid precursor protein
CC (APP) which is an essential step in the production of beta-amyloid. (1)
CC can be used in the treatment and prevention of neurodegenerative diseases
CC such as dementia and Alzheimer's disease. The present sequence represents
CC the A beta 1-40 amino acid sequence which is used in an example from the
CC present invention
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
XX
RESULT 59
AAU96895
ID AAU96895 standard; peptide; 40 AA.
XX
AC AAU96895;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human self-associating Amyloid beta 1-40 peptide.
XX
KM Human; amyloid beta; cell death; neuron death; Alzheimer's disease;
KW neurotropic; neuroprotective; apoptotic.
XX
OS Homo sapiens.

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XX
XX JP2002105099-A.
XX
XX 10-APR-2002.
XX
XX 28-SEP-2000; 2000JP-00295577.
XX
XX 28-SEP-2000; 2000JP-00295577.
XX
XX (MITU ) MITSUBISHI CHEM CORP.
XX
XX WPI; 2002-458303/49.
XX
XX A self-associating type amyloid beta protein.
XX
XX Example 1; Page 9; 14pp; Japanese.
XX
XX The invention relates to a self-associating type amyloid beta protein of
XX particle form having an activity of inducing cell death in nervous system
XX cells at a protein concentration of not higher than 1 micro g/ml. Also
XX included are (1) a method for the preparation of a solution containing a
XX self-associating type amyloid beta protein having high toxicity including
XX a step of connecting aqueous solution containing the amyloid beta protein
XX and a step of fractionating the solution containing the self-associating
XX type amyloid beta protein in the convected aqueous solution; (2) a
XX reagent containing the above self-associating type amyloid beta protein;
XX (3) a method for inducing cell death in nervous system cells by using the
XX above self-associating type amyloid beta protein; (4) a method for
XX screening a drug having inhibiting activity on neuron death; a substance
XX having an inhibiting activity on neuron death prepared by the above
XX method; and (6) a drug for preventing and/or treating Alzheimer's disease
XX for preventing the above substance as the active component. The drug is used
XX for preventing and/or treating Alzheimer's disease. The present sequence
XX is a human amyloid beta 1-40 peptide used in an example demonstrating
XX preparation of the particle of the invention
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
XX
RESULT 60
AAM50909
ID AAM50909 standard; protein; 40 AA.
XX
AC AAM50909;
XX
DT 07-MAY-2002 (first entry)
XX
DE Beta amyloid protein amino acid residues 1-40.
XX
KM Beta amyloid protein; beta/A4; amyloidosis; Alzheimer's disease;
KW amyloid deposition; human; animal model.
XX
OS Homo sapiens.
XX
PN US6340783-B1.
XX
PD 22-JAN-2002.
XX
PF 03-OCT-1996; 96US-00723661.
XX
PR 23-SEP-1992; 92US-00950417.
XX
PR 23-OCT-1992; 92US-00969734.
XX
PR 05-UN-1995; 95US-00461216.
XX
PA (UNITW ) UNIT WASHINGTON.

```

XX Snow AD;
PI
XX WPI; 2002-146857/19.
XX
XX Rodent models for studying amyloid deposition in Alzheimer's disease and
PT for identifying candidate therapeutic agents.
XX
XX Disclosure; Col 67; 78pp; English.
XX
CC The present sequence is that of a protein comprising amino acids 1-40 of
CC beta amyloid protein (or beta/A4). The invention provides a method for
CC producing a rodent (especially rat) model of Alzheimer's disease, which
CC involves infusing a proteoglycan and a beta-amyloid protein into the
CC brain (preferably the hippocampus) of the rodent for a time sufficient to
CC allow co-deposition, and detecting the amyloid deposit in the brain
CC tissue using staining techniques (Congo Red or thioflavin S) for
CC fibrillar amyloid. The beta amyloid protein is preferably comprised of 39
CC and fold into a specific beta-plated sheet. This can be observed using
CC Congo Red staining. Inhibition of staining indicates that an inhibitor
CC has altered the secondary structure of the amyloid protein. In an in vivo
CC assay for selecting a candidate structure of the amyloid protein, the
CC amyloid deposition/persistence in the brain, the candidate reagent is
CC administered to a rodent in an infusate comprising beta/A4 peptide and
CC perlecan by continuous infusion for at least 1 week into the hippocampus.
CC The candidate reagent is selected as a candidate therapeutic for
CC congothilic and fibrillar beta/A4 amyloid deposition in the brain if the
CC infusate diminishes Congo Red and thioflavin S staining indicative of
CC amyloid deposition adjacent to the infusion site as compared to a control
CC rodent receiving an infusate not comprising the candidate reagent. The
CC Alzheimer's disease, and to identify therapeutic agents (e.g. heparin,
CC heparan sulfate, glycosaminoglycans and related macromolecules and heparin
CC binding peptides) that may be used for the treatment of Alzheimer's and
CC other amyloidosis diseases
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 61
AAU80186
ID AAU80186 standard; peptide; 40 AA.
XX
XX AAU80186;
XX
XX 15-JUL-2002 (first entry)
XX
XX Amyloid beta peptide residues 1-40.
XX
XX Amyloid beta; Alzheimer's disease; familial Alzheimer's disease;
XX Down's syndrome; apolipoprotein E4; neurotropic; neuroprotective;
XX thioflavin; polycyclic compound.
XX
XX unidentified.
XX
XX OS
XX WO200216333-A2.
XX
XX PD 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-US026427.
XX
XX 24-AUG-2000; 2000US-0227601P.
XX
XX (UIPI-) UNIV PITTSBURGH.

XX Klunk WE, Mathis CA, Wang Y;
PI
XX WPI; 2002-382815/41.
XX
XX New thioflavin derivatives, useful as amyloid binding agents for in vivo
PT imaging of amyloid deposits.
XX
XX Disclosure; Page 51; 11pp; English.
XX
CC The invention relates to amyloid binding polycyclic derivatives
CC especially thioflavin derivatives. The full structures of the compounds
CC are given in the specification. Also included are methods for making the
CC compounds; compositions for in vivo imaging of amyloid deposits
CC comprising the novel compounds and an in vivo method for detecting
CC amyloid deposits. The compounds show a KD for binding to Amyloid beta 1-
CC 40 peptide of 0.0001 to 10µM. The compounds are useful for in vivo
CC imaging of amyloid deposits. The compounds are also useful for treating
CC Alzheimer's disease, familial Alzheimer's disease, Down's syndrome and
CC conditions associated with apolipoprotein E4 alleles. The present
CC sequence is the amyloid beta 1-40 peptide used to test the compounds of
CC the invention
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 62
AAE26332
ID AAE26332 standard; peptide; 40 AA.
XX
XX AAE26332;
XX
XX 14-NOV-2002 (first entry)
XX
XX Human beta-amyloid peptide mutant (Abeta residues 1-40).
XX
XX Human amyloidogenic protein; Alzheimer's disease; Huntington's disease;
XX spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;
XX Gerstmann-Strausler-Scheinker syndrome; spongiform encephalopathy; GSS;
XX Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;
XX CU; beta-amyloid; mutant; mutlein.
XX
XX Homo sapiens.
XX
XX OS
XX Synthetic.
XX
XX WO200242462-A2.
XX
XX 30-MAY-2002.
XX
XX 27-NOV-2001; 2001WO-US044581.
XX
XX 27-NOV-2000; 2000US-0253302P.
XX
XX 29-NOV-2000; 2000US-0250198P.
XX
XX 20-DEC-2000; 2000US-0257186P.
XX
XX (PRAE-) PRAECTIS PHARM INC.
XX
XX Geffter ML, Israel DI, Uoyal JL, Gosselin M;
XX
XX WPI; 2002-636427/68.
XX
XX Novel therapeutic agent useful for treating an amyloidogenic disorder,
PT e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain
PT constant region linked to a peptide capable of binding amyloidogenic
PT protein.

XX PS Claim 18; Page; 79pp; English.

CC CC The invention relates to a compound comprising an immunoglobulin (Ig)
CC heavy chain constant region or its fragment that retains the ability to
CC bind an Fc receptor linked by a linker group or a direct bond to a
CC peptide capable of binding an amyloidogenic protein. The invention is
CC useful for clearing an amyloidogenic protein such as beta-amyloid,
CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide
CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light
CC chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,
CC gelsolin, calcitonin, fibrinogen, Huntingtin, alpha-synuclein and
CC lysozyme from a subject and for treating an amyloidogenic disorder such
CC as Alzheimer's disease and spongiform encephalopathy. Disorders treatable
CC include those caused or characterised by deposits of TTR (eg. familial
CC amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including
CC scrapie in sheep, bovine spongiform encephalopathy in cows and
CC Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker
CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),
CC ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg.
CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I
CC (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.
CC familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal
CC amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis). Other
CC examples of amyloidogenic disorders include Huntington's disease and
CC inclusion body myocytia. The present sequence is human beta-amyloid
CC peptide mutant. Note: This sequence is not shown in the specification but
CC is derived from human beta-amyloid peptide shown as SEQ ID NO: 1
CC (AAE26265) in the specification

XX SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 63
AAM51863
ID AAM51863 standard; protein; 40 AA.
XX
AC AAM51863;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human amyloid beta protein.
XX
KM Human; amyloid beta; neurone death inhibition; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN JP2001255318-A.
PD 21-SEP-2001.
XX
PF 09-MAR-2000; 2000JP-00064984.
XX
PR 09-MAR-2000; 2000JP-00064984.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI; 2002-003272/01.
XX
PT Screening method for identifying drugs which inhibit neuron cell death
PT comprises culturing the cells, exposing to high concentrations of self-
PT associating beta amyloid protein, and assessing the inhibitory action of
XX the drug on cell death.
XX
PS Example; Page 7; 11pp; Japanese.

XX CC The present invention relates to a method of screening drugs that exhibit
CC inhibitory action on neurone death, involving culturing neuronal cells,
CC exposing them to a self-associating type amyloid beta protein of high
CC toxicity, and assessing if the sample has had an inhibitory action on
CC neurone death when the cell death of said nervous system cells or nervous
CC system organs is inhibited. The method is used for screening a drug
CC having inhibitory action on neurone death, which can then be used to
CC treat Alzheimer's disease. The present sequence is the human amyloid beta
CC protein

XX SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 64
ABU08710
ID ABU08710 standard; protein; 40 AA.
XX
AC ABU08710;
XX
DT 18-JUN-2003 (first entry)
XX
DE Amyloid beta protein 40 (Abeta 40).
XX
KM Amyloid beta; Abeta; amyloid beta A; neurotropic; neuroprotective;
KM gene therapy; Alzheimer's disease.
XX
OS Unidentified.
XX
PN WO2003012141-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002WO-JP000836.
XX
PR 31-JUL-2001; 2001JP-00266510.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
PA (NICH-) JAPAN SEC CHUBU NAT HOSPITAL.
PA (KOMA/) KOMANO H.
XX
PI Komano H;
XX
DR WPI; 2003-239531/23.
XX
PT Screening gene controlling production of amyloid Beta, applicable in
PT diagnosis of and developing drugs for Alzheimer's disease.
XX
PS Disclosure; Page 101; 115pp; Japanese.
XX
XX The invention describes a method of screening a DNA controlling the
CC production of amyloid protein (Abeta) by transferring a DNA library into
CC a cell line with enhancement of expression of a selection marker gene in
CC promoting the Abeta production from a precursor protein (betaAPP)
CC fragment of Abeta, then identifying a DNA clone for transferring into a
CC cell to enhance Abeta production. The methods are useful for screening
CC genes that control production of amyloid beta. The genes, encoded protein
CC and related DNA materials are useful in the diagnosis and development of
CC drugs for Alzheimer's disease. This is the amino acid sequence of amyloid
CC beta protein 40 (Abeta 40), a 40 residue amyloid beta protein fragment

XX SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

Db

RESULT 65
 AB008508
 ID AB008508 standard; peptide; 40 AA.

AC AB008508;

DT 22-MAY-2003 (first entry)

DE Human amyloid beta peptide (1-40).

KW Human; amyloid beta peptide (1-40); Alzheimer's disease; antigen; Abeta.

OS Homo sapiens.

PN US2002182660-A1.

PD 05-DEC-2002.

PF 18-JAN-2002; 2002US-00051496.

PR 18-FEB-2000; 2000US-0183407P.

PR 16-FEB-2001; 2001US-00784854.

XX (FONG/) FONG K. L.

XX Fong KL;

XX WPI, 2003-328616/31.

PT Enabling measurement of full length beta-amyloid peptide level for tracking progression of Alzheimer's disease, comprises capturing and binding terminus of beta-amyloid peptide with antibodies.

PS Disclosure; Fig 1d; 11pp; English.

CC The invention relates to a measurement of the full length beta-amyloid (Abeta) peptide level of a specific Abeta peptide in a sample containing multiple types of Abeta peptide, by capturing and binding one terminus of the types of Abeta peptides with a first antibody. The specific Abeta peptide is captured and bound at an opposite non-overlapping full length with a second peptide. The invention is used for measuring full length Abeta peptide level useful for tracking the progression of Alzheimer's disease. The new method uses one specific antibody that recognizes the N-terminus of all the Abeta peptides and a panel of detection antibodies 1-35) that distinguish each Abeta peptide (Abeta 1-43, 1-42, 1-41, 1-40 and 1-39) by their sequence difference at the C-terminus. This use of N and C-terminal specific antibodies allows simultaneous quantification of several Abeta peptides in a single assay. The present sequence is that of Abeta (1-40), used to raise the N and C-terminal antibodies of the invention

CC Sequence 40 AA;

Query Match 100.0%; Score 162; DB 6; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 66

AA019885

XX AA019885 standard; peptide; 40 AA.

AC AA019885;

DT 11-AUG-2003 (first entry)

DE Human amyloid precursor protein APP immunogenic peptide #5.

KW Human; APP; amyloid precursor protein; immunogen; Alzheimer's disease; high-throughput screening; neuroprotective; nootropic; antiparkinsonian.

OS Homo sapiens.

PN WO2003001881-A2.

PD 09-JUN-2003.

PF 26-JUN-2002; 2002WO-US020267.

PR 26-JUN-2001; 2001US-0300959P.

XX (NYME-) NEW YORK STATE OFFICE MENTAL HEALTH.

XX Mathews PM, Nixon RA, Schmidt SD, Jiang Y;

XX WPI, 2003-210182/20.

PT Identifying compounds that modulates the generation of metabolites associated with a disease or disorder, for treating e.g. Alzheimer's disease by determining levels of a cellular component protein, or its conformation state.

PS Example 1; Page 29; 69pp; English.

CC The present invention relates to a method of identifying compounds that modulate the generation of one or more metabolites associated with a disease or disorder comprising determining levels of a cellular component protein or a conformation state of a cellular precursor protein. In particular, the method can be used to determine levels of amyloid CC precursor protein (APP), which is associated with Alzheimer's disease. It is also useful for identifying compounds as drugs for treating diseases CC or disorders associated with metabolic and/or proteolytic pathways, e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, lysosomal storage disorders, prion diseases, the tau-based neurodegenerative CC disorders, and other non-AD amyloidoses. The present sequence is an immunogenic portion of human APP

CC Sequence 40 AA;

Query Match 100.0%; Score 162; DB 6; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 67

ABP96147
 ID ABP96147 standard; peptide; 40 AA.

AC ABP96147;

DT 12-MAY-2003 (first entry)

DE Human Abeta40 amino acid sequence SEQ ID NO:4.

XX Human; Abeta40; amyloid toxicity inhibition; amyloid; integrin subunit; integrin; laminin; nootropic; neuroprotective; antidiabetic;

KW antiparkinsonian; gene therapy; amyloidogenic protein; prion infection; amyloidogenic protein toxicity inhibition; amyloidogenic disease;

KW Alzheimer's disease; type II diabetes; Parkinson's disease; amyloidosis;

XX Down's syndrome.

OS Homo sapiens.
 XX WO2003006893-A2.
 XX
 XX 23-JAN-2003.
 PD
 XX 08-JUL-2002; 2002WO-US019803.
 XX
 XX 09-JUL-2001; 2001US-0304315P.
 PR 17-DEC-2001; 2001US-0341772P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA
 XX Premier IG, Wright S, Yednock T, Rydel R;
 PI WPI, 2003-221770/21.
 DR
 XX Inhibiting amyloid toxicity or the formation of an amyloid deposit,
 PT comprises administering an agent that binds to an integrin, integrin
 PT subunit, or laminin.
 XX
 XX Disclosure; Page 85; 86pp; English.
 PS
 XX The present invention describes a method for inhibiting amyloid toxicity
 CC or the formation of an amyloid deposit. The method comprises
 CC administering a dosage of one or more agent(s) that bind(s) to a molecule
 CC selected from an integrin subunit such as alpha2, alphaV, alpha6 or
 CC beta1, an integrin such as alpha2beta1, alpha6beta1 or alphaVbeta1, and
 CC laminin, under conditions such that the agent(s) inhibit amyloid toxicity
 CC or the formation of an amyloid deposit. Amyloids have neurotropic,
 CC neuroprotective, antidiabetic and antiparkinsonian activities, and can be
 CC used in gene therapy. The method is useful for inhibiting amyloidogenic
 CC protein toxicity, inhibiting the formation of an amyloidogenic protein
 CC deposit and/or treating amyloidogenic diseases, such as Alzheimer's
 CC disease, type II diabetes, Parkinson's disease, a disease caused all or
 CC in part by prion infection, hereditary or systemic amyloidosis, or Down's
 CC syndrome. The present sequence represents a human Abeta peptide
 CC designated Abeta40, which is given in the exemplification of the present
 CC invention
 XX
 XX Sequence 40 AA;
 SQ
 Query Match 100.0%; Score 162; DB 6; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 RESULT 68
 AAE35429
 ID AAE35429 standard; protein; 40 AA.
 XX
 AC AAE35429;
 XX
 XX 17-JUN-2003 (first entry)
 DT
 XX
 DE Abeta protein #2.
 XX
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cyrostatic; uropathic; therapy.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1. .40
 FT

FT /note= "D-form residues"
 XX
 XX WO200296937-A2.
 XX
 XX 05-DEC-2002.
 PD
 XX 29-MAY-2002; 2002WO-CA000763.
 XX
 XX 29-MAY-2001; 2001US-00867847.
 PR
 XX (NEUR-) NEUROCHEM INC.
 PA
 XX Gervais F, Hebert L, Chailfour RJ, Kong X;
 PI WPI, 2003-201269/19.
 DR
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 58; 44pp; English.
 PS
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta protein used to illustrate the method of the
 CC invention
 XX
 XX Sequence 40 AA;
 SQ
 Query Match 100.0%; Score 162; DB 6; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
 RESULT 69
 ABP60626
 ID ABP60626 standard; peptide; 40 AA.
 XX
 AC ABP60626;
 XX
 XX 27-MAR-2003 (first entry)
 DT
 XX
 DE Human A-beta peptide #2.
 XX
 XX Human; A-beta; Alzheimer's disease; pre-amyloid deposit;
 KW magnetic resonance imaging.
 KW
 XX Homo sapiens.
 OS
 XX WO200294191-A2.
 PN
 XX 28-NOV-2002.
 PD
 XX 23-MAY-2002; 2002WO-US016057.
 PF
 XX

CC or neprylasin, within the brain of the affected individuals. The sequence
CC presented is the Abeta1-40 peptide
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGKGA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGKGA 30
RESULT 74
ADA37266 standard; protein; 40 AA.
XX ADA37266;
XX 20-NOV-2003 (first entry)
XX Human beta-amyloid precursor protein 597-636 SEQ ID NO:1.
XX
XX amyloid-beta peptide related disorder; Abeta-related disorder;
XX adenosine triphosphate dependent enzyme activity modulator;
XX ATP-dependent enzyme activity modulator; ATP modulator; neurotropic;
XX neuroprotective; Alzheimer's disease; senile dementia; Down's syndrome;
XX inclusion body myositis; memory loss; mild cognitive impairment;
XX cognitive decline; severe cognitive impairment; personality change;
XX human; beta-amyloid precursor protein; APP.
XX
XX Homo sapiens.
XX
XX WO2003057165-A2.
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000249.
XX
XX 04-JAN-2002; 2002US-0345009P.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Netzer WJ, Greengard P, Xu H;
XX WPI, 2003-645970/61.
XX
XX Treatment or amelioration of symptom of amyloid-beta peptide-related
XX disorder e.g. Alzheimer's disease comprises administration of an
XX adenosine triphosphate (ATP)-dependent enzymatic activity modulator or an
XX ATP modulator.
XX
XX Disclosure, Page 72; 142p; English.
XX
XX The present invention describes a method for the treatment or
XX amelioration of symptoms of an amyloid-beta peptide (Abeta)-related
XX disorder, which involves the administration of an adenosine triphosphate
XX (ATP)-dependent enzyme activity modulator or ATP modulator (A). (A) has
XX neurotropic and neuroprotective activities. The method is used for treating
XX or ameliorating a symptom of an Abeta-related disorder e.g. Alzheimer's
XX disease in a subject e.g. human, who is at risk for familial form of
XX Alzheimer's disease. (A) can also be used for the treatment of senile
XX dementia, Down's syndrome, inclusion body myositis, memory loss, mild
XX cognitive impairment, cognitive decline, severe cognitive impairment and
XX personality changes that result in loss of functional ability. The
XX present sequence represents a human beta-amyloid precursor protein (APP)
XX amino acid sequence of residues 597 to 636, corresponding to Abeta 1-40,
XX which is given in the exemplification of the present invention.
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 7; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGKGA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGKGA 30
RESULT 75
ADB85563 standard; peptide; 40 AA.
XX ADB85563;
XX 04-DEC-2003 (first entry)
XX Beta-amyloid peptide Abeta1-40 related to Alzheimer's disease treatment.
XX
XX Alzheimer's disease; neuronal cell; membrane depolarisation;
XX beta-amyloid protein; neurotropic; neuroprotective;
XX neuronal cell dysfunction; neuronal cell loss; cytotoxic mechanism;
XX beta-amyloid peptide aggregation; calcium homeostasis; human; Abeta1-40.
XX
XX Homo sapiens.
XX
XX US2003105152-A1.
XX
XX 05-JUN-2003.
XX
XX 10-MAY-2002; 2002US-00143534.
XX
XX 03-NOV-2000; 2000US-00706574.
XX 18-JAN-2002; 2002US-00051663.
XX
XX (INGR/) INGRAM V M.
XX (BLAN/) BLANCHARD B J.
XX (STOC/) STOCKWELL B R.
XX
XX Ingram VM, Blanchard BJ, Stockwell BR;
XX WPI, 2003-635483/60.
XX
XX Treating Alzheimer's disease comprises contacting neuronal cell with
XX composition comprising compound reducing membrane depolarization of
XX neuronal cells.
XX
XX Disclosure, Page 20; 34p; English.
XX
XX This invention relates to a novel method of treating Alzheimer's disease
XX and comprises contacting a neuronal cell with a composition comprising at
XX least one compound that reduces membrane depolarisation of neuronal cells
XX caused by aggregated beta-amyloid protein degradation products. The
XX compounds of the invention may have neurotropic or neuroprotective
XX activities. Beta-amyloid peptides are neurotoxic and are believed to
XX cause neuronal cell dysfunction and cell loss characteristic of
XX Alzheimer's disease. Identification of the cytotoxic mechanisms involving
XX beta-amyloid peptides may provide a method of designing compounds capable
XX of antagonising the effects of aggregation of beta-amyloid peptides and
XX that of a human beta-amyloid peptide related. The present sequence is
XX used as a model peptide for investigating the role of beta-amyloid
XX peptides on calcium homeostasis in neuronal cells.
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGKGA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGKGA 30

```

RESULT 76
AAE38648
ID AAE38648 standard; peptide; 40 AA.
XX
AC AAE38648;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human amyloid-beta peptide #1.
XX
KW Human; therapy; osteoporosis; left-ventricular hypertrophy; scleroderma;
KW liver cirrhosis; congestive heart failure; multiple sclerosis; fibrosis;
KW coal-miner's pneumoconiosis; muscle-wasting syndrome; diabetes mellitus;
KW rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer;
KW amyloid-beta.
XX
OS Homo sapiens.
XX
PN WO2003068919-A2.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-US004183.
XX
PR 12-FEB-2002; 2002US-0356008P.
XX
PA (RBGC ) UNIV CALIFORNIA.
XX
PI Hellerstein MK;
XX
DR WPI; 2003-689661/65.
XX
PT Determining rate of biosynthesis or breakdown of inaccessible biological
PT molecules, useful e.g. for diagnosis or monitoring treatment, by
PT administering labeled precursor.
XX
PS Disclosure; Page 105; 105pp; English.
XX
CC The invention relates to a method of determining the rate of biosynthesis
CC or breakdown of at least one inaccessible biological molecule in a
CC subject. The method is useful for diagnosis or monitoring and treatment
CC of diseases associated with an altered rate of biosynthesis/breakdown of
CC an isotopically labelled precursor molecule, specifically osteoporosis;
CC left-ventricular hypertrophy; liver cirrhosis or fibrosis; congestive
CC heart failure; scleroderma; coal-miner's pneumoconiosis; cardiac or lung
CC fibrosis; Alzheimer's disease; multiple sclerosis; rheumatoid arthritis;
CC diabetes mellitus; muscle-wasting syndromes; muscular dystrophy; athletic
CC training and cancer. The method is also useful for screening candidate
CC gene or protein targets, phenotypic/human validation studies on potential
CC drugs, drug mechanism studies and determining the risk of developing the
CC disease. The present sequence is human amyloid-beta peptide. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 40 AA;
QY
Query Match 100.0%; Score 162; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

```

```

DE Human A(Beta)40.
XX
KW Human; amyloid beta protein; XB31 alpha; XB31 beta; Alzheimer's disease;
KW X11L; APPbeta; XB51; A(beta)40.
XX
OS Homo sapiens.
XX
PN JP2003164298-A.
XX
PD 10-JUN-2003.
XX
PF 30-NOV-2001; 2001JP-00367100.
XX
PR 30-NOV-2001; 2001JP-00367100.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
PA (SUZU/) SUZUKI Y.
XX
DR WPI; 2003-611388/58.
XX
PT Screening of compound that inhibits production of amyloid beta protein or
PT its salt used in pharmaceutical for preventing Alzheimer's disease,
PT involves using alpha or beta XB31.
XX
PS Disclosure; SEQ ID NO 11; 41pp; Japanese.
XX
CC The present invention relates to a method for screening compounds that
CC inhibit production of amyloid beta protein or its salt using XB31
CC alpha/beta, X11L, APPbeta or XB51 (AD65591-AD66000). The compound is
CC useful in a pharmaceutical and composite or its salt. The pharmaceutical
CC is used as therapeutic agent for treating Alzheimer's disease. The
CC present sequence was used to illustrate the invention.
XX
SQ Sequence 40 AA;
QY
Query Match 100.0%; Score 162; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

```

```

RESULT 78
ADC35182
ID ADC35182 standard; peptide; 40 AA.
XX
AC ADC35182;
XX
DT 18-DEC-2003 (first entry)
XX
DE Beta-amyloid peptide Abeta1-40.
XX
KW Beta-amyloid peptide; Abeta1-40; Alzheimer's disease; neuronal cell;
KW membrane depolarisation; aggregated beta-amyloid; Abeta; calcium influx;
KW secretase inhibitor; tyrosine kinase inhibitor;
KW chloride channel antagonist; dopamine receptor antagonist;
KW alpha-adrenergic receptor antagonist; lead compound;
KW neuronal membrane depolarisation; Abeta aggregate; nootropic;
KW neuroprotective.
XX
OS Synthetic.
XX
PN US2003114510-A1.
XX
PD 19-JUN-2003.
XX
PF 18-JAN-2002; 2002US-00051663.
XX
PR 03-NOV-2000; 2000US-00706574.
XX
PA (INGR/) INGRAM V M.

```

PA (BLAN/) BLANCHARD B J.
PA (STOC/) STOCKWELL B R.
XX Ingram VM, Blanchard BJ, Stockwell BR;
PT WPI; 2003-696325/66.
XX
XX
XX Treating Alzheimer's disease by contacting neuronal cell with composition
PT comprising compound that decreases membrane depolarization of neuronal
PT cells caused by aggregated beta-amyloid protein degradation products.
XX
XX
XX Disclosure; SEQ ID NO 3; 33bp; English.
XX
XX The invention relates to a method for treating Alzheimer's disease
CC comprising contacting a neuronal cell with a pharmaceutical composition
CC comprising compound(s) that decreases membrane depolarization of neuronal
CC cells caused by aggregated beta-amyloid (Abeta) protein degradation
CC products. The invention also relates to a pharmaceutical composition
CC comprising compound(s) that decreases membrane depolarization of neuronal
CC cells, compound(s) that decreases calcium influx of neuronal cells, and a
CC secretase inhibitor, treating a subject having a condition characterised
CC by neuronal membrane depolarisation comprising administering a
CC composition comprising a tyrosine kinase inhibitor, a chloride channel
CC antagonist, a dopamine receptor antagonist or an alpha-adrenergic
CC receptor antagonist, and identifying lead compounds for a pharmacological
CC agent, e.g. a peptide or small organic molecule, useful in the treatment
CC of conditions associated with increased neuronal depolarisation induced
CC by the presence of Abeta aggregates. The method is used for treating
CC Alzheimer's disease and conditions characterised by neuronal membrane
CC depolarisation and for identifying lead compounds for pharmacological
CC agents. This sequence represents a beta-amyloid peptide of the invention.
XX
XX
XX Sequence 40 AA;
SQ

Query Match 100.0%; Score 162; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

RESULT 79
ADF55648 ID ADF55648 standard; peptide; 40 AA.
XX
XX ADF55648;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human A beta 1-40.
DE
XX
XX amyloid plaque; neurotoxicity; amyloid peptide inactivating enzyme;
XX Alzheimer's disease; human; A beta 1-40.
KW
XX
XX Homo sapiens.
OS
XX
XX US2003165481-A1.
PN
XX
XX 04-SEP-2003.
PD
XX
XX 03-JUN-2002; 2002US-00159279.
PF
XX
XX 24-FEB-2000; 2000US-0184826P.
PR
XX
XX 26-FEB-2001; 2001US-00792079.
PR
XX
XX (HERS/) HERSH L B.
PA
XX
XX Hersh LB;
PI
XX
XX WPI; 2003-898030/82.
DR
XX

PT Preventing formation or growth of amyloid plaques without causing
PT neurotoxicity; useful for treating Alzheimer's disease; by generating a
PT vector comprising a DNA sequence encoding at least one amyloid peptide
PT inactivating enzyme.
XX
XX
XX Disclosure; SEQ ID NO 12; 36bp; English.
XX
XX
XX The invention relates to a method of preventing formation or growth of
CC amyloid plaque without causing neurotoxicity which comprises generating a
CC recombinant viral or plasmid vector comprising a DNA sequence encoding at
CC least one amyloid peptide inactivating enzyme operably linked to a
CC promoter. The methods are useful for treating Alzheimer's disease by
CC increasing the activity of an amyloid inactivating enzyme. The present
CC sequence represents the amino acid sequence of human A beta 1-40.
XX
XX
XX Sequence 40 AA;
SQ

Query Match 100.0%; Score 162; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

RESULT 80
ADK82702 ID ADK82702 standard; peptide; 40 AA.
XX
XX ADK82702;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Beta-amyloid peptide #8 recognised by antibody to treat senile dementia.
DE
XX
XX fusion antibody; senile dementia; beta-amyloid peptide; fibre;
XX immunocell.
KW
XX
XX Homo sapiens.
OS
XX
XX CN1396183-A.
PN
XX
XX 12-FEB-2003.
PD
XX
XX 13-JUL-2001; 2001CN-00120278.
PF
XX
XX 13-JUL-2001; 2001CN-00120278.
PR
XX
XX (ZHAN/) ZHANG X.
PA
XX
XX Zhang X, Zhang J;
PI
XX
XX WPI; 2003-442233/42.
DR
XX
XX Human fusion antibody for reducing cerebral amyloid fibers associated
XX with senile dementia.
PT
XX
XX Claim 1; Page 2; 26pp; Chinese.
XX
XX The invention relates to a human fusion antibody for preventing and
CC treating senile dementia. The antibody recognises and binds the beta-
CC amyloid peptide and the fibres generated by it. The human antibody Fc
CC segment recognized by human immunocells are sequentially contained by its
CC terminals from N to C. The fusion gene coding for the antibody is also
CC disclosed. This sequence represents a beta-amyloid peptide recognised by
XX the antibody.
XX
XX
XX Sequence 40 AA;
SQ

Query Match 100.0%; Score 162; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30
|||
Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 81

ADFS3270
ID ADFS3270 standard; protein; 40 AA.

AC ADFS3270;

DT 12-FEB-2004 (first entry)

DE Amyloid A(beta)40 amino acid sequence.

KM amyloid A(beta); beta-amyloid precursor protein; APP;
KW Alzheimer's disease; neurodegenerative disease; Down's syndrome;
XX Parkinson's disease; amyotrophic lateral sclerosis; diabetic neuropathy.

OS Homo sapiens.

PN JP2003289881-A.

PD 14-OCT-2003.

PF 31-JUL-2002; 2002JP-00223200.

PR 31-JUL-2001; 2001JP-00266510.

PR 01-FEB-2002; 2002JP-00025878.

PA (KOKU-) KOKURITSU RYOYOJO CHUBU BYOINCHO.

PA (KOMA/) KOMANO H.

PA (TAKS) TAKEDA CHEM IND LTD.

DR WPI; 2004-038437/04.

XX Screening of DNA controlling amyloid beta protein production by

PT transducing DNA that promotes amyloid beta production from precursor

PT protein, into cell, identifying transduced clone which enhances the

PT production.

XX Disclosure; SEQ ID NO 18; 48pp; Japanese.

XX The invention relates to a method of screening for DNA which controls

CC production of amyloid A(beta) protein, comprising transducing a DNA

CC library which promotes the production of A(beta) protein from beta-

CC amyloid precursor protein (APP) protein, into the cell strain, so that

CC expression of selective-marker gene is enhanced, and identifying the

CC transduced clone which enhances the production of A(beta). The method is

CC useful for screening DNA that controls production of A(beta) protein.

CC Nucleic acid sequences that control this expression, antibodies to the

CC proteins, antisense nucleic acids and inhibitors of the proteins are

CC useful for diagnosing and treating Alzheimer's disease. The antisense

CC nucleic acids and inhibitors are also useful for treating

CC neurodegenerative diseases such as Down's syndrome, Parkinson's disease,

CC amyotrophic lateral sclerosis, diabetic neuropathy, etc. This sequence

CC corresponds to the amino acid sequence of the amyloid A(beta)40 protein.

XX SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 8; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.9e-18; Mismatches 0; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30
|||
Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 82

ADN00693
ID ADN00693 standard; protein; 40 AA.

XX ADN00693;
AC 17-JUN-2004 (first entry)
DT A40, SEQ ID 1.

DE A40, SEQ ID 1.

KM Neuroprotective; Vaccine; conformational epitope;
KW protofibrillar aggregate; amyloid fibril; amyloid deposit;
XX Alzheimer's disease; amyloid peptide; A40.

OS Unidentified.

PN WO2004024090-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028829.

PR 12-SEP-2002; 2002US-0410069P.

PA (REGC) UNIV CALIFORNIA.

PI Kayed R, Glabe CG;

DR WPI; 2004-269879/25.

PT New composition comprising a conformational epitope of a protofibrillar
PT aggregate, useful for preventing or treating a disease or condition
PT characterized by the presence of amyloid deposits, e.g. Alzheimer's
PT disease.

XX Claim 5; SEQ ID NO 1; 82pp; English.

XX The present invention relates to an antigenic composition comprising a

CC conformational epitope of a protofibrillar aggregate which forms in a

CC human or animal and contributes to amyloid fibril formation. The

CC composition is useful for preventing or treating a disease or condition

CC characterized by the presence of amyloid deposits, e.g. Alzheimer's

CC disease. The present sequence is an amyloid peptide, which forms an

CC amyloid peptide aggregate which produces a conformational epitope, and

CC was used to illustrate the invention.

XX SQ Sequence 40 AA;

Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30
|||
Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 83

ADN41885
ID ADN41885 standard; peptide; 40 AA.

AC ADN41885;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of beta-amyloid peptide (1-40) variant G37A.

KM Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody.

OS Unidentified.

PN WO2004032868-A2.

PD 22-APR-2004.

PF 09-OCT-2003; 2003WO-US032080.

XX 09-OCT-2002; 2002US-0417232P.
PR 13-FEB-2003; 2003US-0447611P.
PR 22-APR-2003; 2003US-0464754P.
PR 20-JUN-2003; 2003US-0480353P.
PA (RINA-) RINAT NEUROSCIENCE CORP.
PI Rosenthal A, Levkowitz G;
XX WPI; 2004-340802/31.
DR WPI; 2004-340802/31.
XX
XX Treating or preventing diseases associated with expression of amyloid-
PT beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises
PT administering an amount of an antibody directed against amyloid-beta
PT peptide.
XX
XX Example 2; Page 71; 89pp; English.
PS
XX The specification describes a method for treating Alzheimer's disease.
CC The method comprises administering to a subject a pharmaceutical
CC composition comprising an antibody that binds preferentially to amino
CC acids 28-40 of beta-amyloid peptide (1-40). The method is useful for
CC diagnosing, treating or preventing diseases associated with expression of
CC amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The
CC present sequence represents a beta-amyloid peptide (1-40) variant, with
CC the change G37A. It was used to test antibodies of the invention.
XX
SQ Sequence 40 AA;
XX
XX Query Match 100.0%; Score 162; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
XX
XX RESULT 84
ID ADN41881 standard; peptide; 40 AA.
XX
XX ADN41881;
AC
XX 15-JUL-2004 (first entry)
XX
XX Amino acid sequence of beta-amyloid peptide (1-40) variant V39A.
XX
XX Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody.
XX
XX Unidentified.
XX
XX WO2004032868-A2.
XX
XX 22-APR-2004.
XX
XX 09-OCT-2003; 2003WO-US032080.
XX
XX 09-OCT-2002; 2002US-0417232P.
PR 13-FEB-2003; 2003US-0447611P.
PR 22-APR-2003; 2003US-0464754P.
PR 20-JUN-2003; 2003US-0480353P.
XX
XX (RINA-) RINAT NEUROSCIENCE CORP.
XX
XX Rosenthal A, Levkowitz G;
XX
XX WPI; 2004-340802/31.
XX
XX Treating or preventing diseases associated with expression of amyloid-
PT beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises
PT administering an amount of an antibody directed against amyloid-beta

PT peptide.
XX
XX Example 2; Page 71; 89pp; English.
PS
XX The specification describes a method for treating Alzheimer's disease.
CC The method comprises administering to a subject a pharmaceutical
CC composition comprising an antibody that binds preferentially to amino
CC acids 28-40 of beta-amyloid peptide (1-40). The method is useful for
CC diagnosing, treating or preventing diseases associated with expression of
CC amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The
CC present sequence represents a beta-amyloid peptide (1-40) variant, with
CC the change V39A. It was used to test antibodies of the invention.
XX
SQ Sequence 40 AA;
XX
XX Query Match 100.0%; Score 162; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
XX
XX RESULT 85
ID ADN41882 standard; peptide; 40 AA.
XX
XX ADN41882;
AC
XX 15-JUL-2004 (first entry)
XX
XX Amino acid sequence of beta-amyloid peptide (1-40) variant V40A.
XX
XX Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody.
XX
XX Unidentified.
XX
XX WO2004032868-A2.
XX
XX 22-APR-2004.
XX
XX 09-OCT-2003; 2003WO-US032080.
XX
XX 09-OCT-2002; 2002US-0417232P.
PR 13-FEB-2003; 2003US-0447611P.
PR 22-APR-2003; 2003US-0464754P.
PR 20-JUN-2003; 2003US-0480353P.
XX
XX (RINA-) RINAT NEUROSCIENCE CORP.
XX
XX Rosenthal A, Levkowitz G;
XX
XX WPI; 2004-340802/31.
XX
XX Treating or preventing diseases associated with expression of amyloid-
PT beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises
PT administering an amount of an antibody directed against amyloid-beta
PT peptide.
XX
XX Example 2; Page 71; 89pp; English.
PS
XX The specification describes a method for treating Alzheimer's disease.
CC The method comprises administering to a subject a pharmaceutical
CC composition comprising an antibody that binds preferentially to amino
CC acids 28-40 of beta-amyloid peptide (1-40). The method is useful for
CC diagnosing, treating or preventing diseases associated with expression of
CC amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The
CC present sequence represents a beta-amyloid peptide (1-40) variant, with
CC the change V40A. It was used to test antibodies of the invention.
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 162; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30
 ||||||||||||||||||||||||||||||||
 Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 86

ADN41884
 ID ADN41884 standard; peptide; 40 AA.

AC ADN41884;

DT 15-JUN-2004 (first entry)

DE Amino acid sequence of beta-amyloid peptide (1-40) variant V36A.

XX Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody.

OS Unidentified.

PN WO2004032868-A2.

PD 22-APR-2004.

PF 09-OCT-2003; 2003WO-US032080.

PR 09-OCT-2002; 2002US-0417232P.

PR 13-FEB-2003; 2003US-0447611P.

PR 22-APR-2003; 2003US-0464754P.

PR 20-JUN-2003; 2003US-0480353P.

PA (RINA-) RINAT NEUROSCIENCE CORP.

PI Rosenthal A, Levkowitz G;

DR WPI; 2004-340802/31.

PT Treating or preventing diseases associated with expression of amyloid-beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises administering an amount of an antibody directed against amyloid-beta peptide.

PS Example 2; Page 71; 89pp; English.

CC The specification describes a method for treating Alzheimer's disease.

CC The method comprises administering to a subject a pharmaceutical composition comprising an antibody that binds preferentially to amino acids 28-40 of beta-amyloid peptide (1-40). The method is useful for diagnosing, treating or preventing diseases associated with expression of amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The present sequence represents a beta-amyloid peptide (1-40) variant, with the change V36A. It was used to test antibodies of the invention.

CC

CC

XX Sequence 40 AA;

Query Match 100.0%; Score 162; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30
 ||||||||||||||||||||||||||||||||
 Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 87

ADN41865
 ID ADN41865 standard; peptide; 40 AA.

AC ADN41865;

XX

DT 15-JUN-2004 (first entry)

DE Amino acid sequence of beta-amyloid peptide (1-40).

XX Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody.

OS Unidentified.

PN WO2004032868-A2.

PD 22-APR-2004.

PF 09-OCT-2003; 2003WO-US032080.

PR 09-OCT-2002; 2002US-0417232P.

PR 13-FEB-2003; 2003US-0447611P.

PR 22-APR-2003; 2003US-0464754P.

PR 20-JUN-2003; 2003US-0480353P.

PA (RINA-) RINAT NEUROSCIENCE CORP.

PI Rosenthal A, Levkowitz G;

DR WPI; 2004-340802/31.

PT Treating or preventing diseases associated with expression of amyloid-beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises administering an amount of an antibody directed against amyloid-beta peptide.

PS Claim 1; Page 70; 89pp; English.

CC The specification describes a method for treating Alzheimer's disease.

CC The method comprises administering to a subject a pharmaceutical composition comprising an antibody that binds preferentially to amino acids 28-40 of beta-amyloid peptide (1-40). The method is useful for diagnosing, treating or preventing diseases associated with expression of amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The present sequence represents a beta-amyloid peptide (1-40), to which antibodies of the invention bind.

CC

CC

XX Sequence 40 AA;

Query Match 100.0%; Score 162; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30
 ||||||||||||||||||||||||||||||||
 Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 88

ADN41880
 ID ADN41880 standard; peptide; 40 AA.

AC ADN41880;

DT 15-JUN-2004 (first entry)

DE Amino acid sequence of beta-amyloid peptide (1-40) variant G38A.

XX Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody.

OS Unidentified.

PN WO2004032868-A2.

PD 22-APR-2004.

PF 09-OCT-2003; 2003WO-US032080.

PR 09-OCT-2002; 2002US-0417232P.

PR 13-FEB-2003; 2003US-044761P.
PR 22-APR-2003; 2003US-046475P.
PR 20-JUN-2003; 2003US-0480353P.
XX
PA (RIMA-) RIMAT NEUROSCIENCE CORP.
PI Rosenthal A, Levkowitz G;
XX WPI; 2004-340802/31.
DR
XX
PT Treating or preventing diseases associated with expression of amyloid-
PT beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises
PT administering an amount of an antibody directed against amyloid-beta
PT peptide.
XX
XX Example 2; Page 71; 89pp; English.
XX
CC The specification describes a method for treating Alzheimer's disease.
CC The method comprises administering to a subject a pharmaceutical
CC composition comprising an antibody that binds preferentially to amino
CC acids 28-40 of beta-amyloid peptide (1-40). The method is useful for
CC diagnosing, treating or preventing diseases associated with expression of
CC amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The
CC present sequence represents a beta-amyloid peptide (1-40) variant, with
CC the change G38A. It was used to test antibodies of the invention.
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
XX
RESULT 89
AD010000
ID AD010000 standard; protein; 40 AA.
XX
AC AD010000;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human beta-amyloid protein (Abeta 1-40) SEQ ID NO:1.
XX
XX amyloid plaque induction; sulphated glycosaminoglycan;
KM low fibrillar Abeta 1-40; LfAbeta; human; beta-amyloid protein;
KM Abeta 1-40; Alzheimer's disease; Parkinson's disease.
XX
XX Homo sapiens.
OS
PN WO2004041779-A2.
XX
PD 21-MAY-2004.
XX
PF 31-OCT-2003; 2003WO-US034797.
XX
PR 01-NOV-2002; 2002US-0423185P.
XX
PA (PROT-) PROTEOTEC INC.
XX
PI Nguyen BP, Choi PY, Sanders VJ, Castillo GM, Snow AD;
XX WPI; 2004-440491/41.
DR
XX
PT Induction of amyloid plaques useful for screening and identification of
PT anti-plaque compounds involves immobilizing sulfated glycosaminoglycan or
PT GAG-related macromolecule on medium followed by adding dissolved low
PT fibrillar.
XX
PS Disclosure; SEQ ID NO 1, 53pp; English.

XX
CC The present invention describes a method for the induction of amyloid
CC plaques. The method comprises (a) immobilising a quantity of a selected
CC selected glycosaminoglycan (SGAG) or a GAG-related macromolecule on a
CC selected medium, and (b) adding to the immobilised SGAG on the medium a
CC quantity of dissolved low fibrillar Abeta 1-40 (LfAbeta). The present
CC sequence represents the human beta-amyloid protein (Abeta 1-40), also
CC known as Abeta 40, which is given in the exemplification of the present
CC invention. The method can be used in the treatment of Alzheimer's disease
CC and Parkinson's disease.
XX
SQ Sequence 40 AA;
XX
Query Match 100.0%; Score 162; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
XX
RESULT 90
AD026239
ID AD026239 standard; peptide; 40 AA.
XX
AC AD026239;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human amyloid-beta peptide.
XX
XX Human; amyloid-beta; amyloid disease; Alzheimer's disease;
KM neuroprotective; nootropic.
XX
XX Homo sapiens.
OS
PN WO2004056318-A2.
XX
PD 08-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-US040744.
XX
PR 19-DEC-2002; 2002US-0434736P.
XX
PA (UTNY) UNITV NEW YORK STATE.
XX
PI Frangione B, Sigurdsson EM, Ghiso J;
XX WPI; 2004-507587/48.
DR
XX
PT Treating patient suffering from amyloid disease e.g. Alzheimer's disease,
PT comprises administering to a patient in need of such treatment, a
PT compound capable of binding to free amyloid beta in body fluid of the
PT patient.
XX
XX Example 1; SEQ ID NO 1, 55pp; English.
XX
CC The present sequence is that of a human amyloid-beta peptide
CC corresponding to amino acid residues 672-711 of the amyloid-beta
CC precursor protein 770. The peptide was used in an example from the
CC invention in which its binding to various forms of apolipoprotein B
CC (apoB) was evaluated. High affinity binding was demonstrated, suggesting
CC that apoB may be useful as an amyloid-beta binding compound for
CC therapeutic purposes. A claimed method of treating a patient suffering
CC from an amyloid disease comprises administering a compound which binds to
CC free amyloid-beta in a body fluid of the patient. The binding complex
CC formed between the compound and amyloid-beta is excreted from the
CC patient. The amyloid disease is especially Alzheimer's disease. Suitable
CC compounds include apoB2, apoB3 and apoB4. Another claimed method of
CC treating an amyloid disease comprises filtering the blood of a patient to
CC remove amyloid-beta. The method uses a membrane, filter or column
CC comprising a bound compound (e.g. apoB) that binds amyloid-beta. The

CC filtered blood is then returned to the patient.
 XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 162; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 DB 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 RESULT 91
 ADQ37253
 ID ADQ37253 standard; peptide; 40 AA.
 XX
 AC ADQ37253;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW neuroprotective; cerebroprotective; immune response; nootropic;
 KW anticholinergic; cardiovascular; haemostatic; ophthalmological;
 KW anticholinergic; anti-HIV; antiparkinsonian; tranquiliser; uteropathic;
 KW candidant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..40
 FT /note= "D-form residues"
 XX
 PN MO2004058239-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 24-DEC-2003; 2003MO-CA002021.
 XX
 PR 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 PA (NEUR-) NEUROCHEM INT LTD.
 XX
 PI Gervais F, Bellini F;
 XX
 DR WPI; 2004-543342/52.
 XX
 PT Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 67; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (1) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have

CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, anticholinergic, vasotropic, cardiovascular, tranquiliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, candidant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an Apol gene, or a presenilin gene,
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 40 AA;
 QY 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 DB 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGA 30
 Query Match 100.0%; Score 162; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 92
 ADRI6410
 ID ADRI6410 standard; peptide; 40 AA.
 XX
 AC ADRI6410;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human Abeta (amyloid-beta) 1-40 peptide.
 XX
 KW Alzheimer's Disease; AD; ocular tissue; lens; amyloidogenic disorder;
 KW Creutzfeldt-Jakob disease; spongiform encephalopathy; Prion disease;
 KW scrapie; bovine spongiform encephalopathy; veterinary prionopathy;
 KW Parkinson's disease; Huntington's disease; trinucleotide repeat disease;
 KW amyotrophic lateral sclerosis; Down's Syndrome; Pick's Disease;
 KW Frontotemporal Dementia; Lewy Body Disease; Hallerorden-Spatz Disease;
 KW synucleinopathy; multiple system atrophy;
 KW neuronal intranuclear inclusion disease; tauopathy;
 KW progressive supranuclear palsy; corticobasal degeneration; human;
 KW amyloid-beta; Abeta.
 XX
 OS Homo sapiens.
 XX
 PN US2004152068-A1.
 XX
 PD 05-AUG-2004.
 XX
 PR 18-NOV-2003; 2003US-00715776.
 XX
 PR 21-AUG-2000; 2000US-0226590P.

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PR 27-APR-2001; 2001US-0287124P.
PR 21-AUG-2001; 2001US-00935126.
PR 25-APR-2002; 2002US-00132779.
PR 18-NOV-2002; 2002US-0427153P.
PR 05-MAR-2003; 2003US-0452336P.
XX
XX (GOLD/) GOLDSTEIN L E.
PA (CHYL/) CHYLACK L T.
XX
XX Goldstein LE, Chylack LT;
XX
XX WPI; 2004-580178/56.
XX
XX Method for diagnosing Alzheimer's disease in a mammal involves contacting
PT an ocular tissue with a detectably-labeled compound that binds to an
PT amyloid protein or use of magnetic resonance imaging.
XX
XX Example 3; Fig 1C; 23pp; English.
XX
CC The invention relates to a method for diagnosing or providing a prognosis
CC regarding the state of Alzheimer's Disease (AD) in a mammal. The method
CC involves contacting an ocular tissue with a detectably-labeled compound
CC that binds to an amyloid protein where an increase in binding of the
CC compound to the ocular tissue compared to the normal control level of
CC binding indicates that the mammal is suffering from or is at risk of
CC developing AD. The method is also used for the diagnosis of amyloidogenic
CC disorder e.g. Familial AD, Sporadic AD, Creutzfeld-Jakob disease, variant
CC Creutzfeld-Jakob disease, spongiform encephalopathies, Prion diseases
CC (including scrapie, bovine spongiform encephalopathy and other veterinary
CC prionopathies), Parkinson's disease, Huntington's disease (and
CC trinucleotide repeat diseases), amyotrophic lateral sclerosis, Down's
CC Syndrome (Trisomy 21), Pick's Disease (Frontotemporal Dementia), Lewy
CC Body Disease, neurodegeneration with brain iron accumulation
CC (Hallervorden-Spatz Disease), synucleinopathies (including Parkinson's
CC disease, multiple system atrophy, dementia with Lewy Bodies, and others),
CC neuronal intranuclear inclusion disease, tauopathies (including
CC progressive supranuclear palsy, Pick's disease, corticobasal
CC degeneration, hereditary frontotemporal dementia (with or without
CC Parkinsonism) and Guam amyotrophic lateral sclerosis/Parkinsonism
CC dementia complex). The present sequence is the human amyloid-beta (Abeta)
CC 1-40 peptide; tryptic peptides derived from this peptide are detected in
CC human lens tissue.
XX
XX Sequence 40 AA;
XX
XX Query Match 100.0%; Score 162; DB 8; Length 40;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-18;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 93
ADSI8445
ID ADSI8445 standard; peptide; 40 AA.
XX
XX ADSI8445;
XX
XX 30-DEC-2004 (first entry)
XX
XX Amyloid-beta inhibitor peptide Abeta1-40, seq id 1.
XX
XX Neuroprotective; neurotrophic; gene therapy; Alzheimer's disease;
XX amyloid-beta; amyloid-beta chaperone; alpha-chymotrypsin;
XX apolipoprotein E; Abeta1-40.
XX
XX Unidentified.
XX
XX OS
XX PN WO2004087733-A2.
XX PD 14-OCT-2004.
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```
XX 26-MAR-2004; 2004WO-US009045.
XX 28-MAR-2003; 2003US-0458986P.
XX (UYNV ) UNIV NEW YORK STATE.
XX Wisniewski T, Sadowski M, Sigurdsson EM;
XX WPI; 2004-729214/71.
XX
XX Preventing or treating Alzheimer's disease in a subject comprises
PT administering to the subject an agent (a peptide or peptidomimetic) that
PT inhibits interaction between amyloid-beta and proteins which chaperone
PT amyloid-beta.
XX
XX Example 1; SEQ ID NO 1; 51pp; English.
XX
CC The invention relates to a method for preventing or treating Alzheimer's
CC disease in a subject, comprising administering to the subject an agent
CC that inhibits interaction between amyloid-beta and proteins which
CC chaperone amyloid-beta under conditions to prevent or treat Alzheimer's
CC disease in the subject. The chaperone proteins are alpha-chymotrypsin or
CC apolipoprotein E. The methods of the invention are useful for preventing
CC and/or treating Alzheimer's disease. The current sequence represents a
CC synthetic peptide that inhibits interaction between amyloid-beta and its
CC chaperone proteins.
XX
XX Sequence 40 AA;
XX
XX Query Match 100.0%; Score 162; DB 8; Length 40;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-18;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 94
ADU24434
ID ADU24434 standard; protein; 40 AA.
XX
XX ADU24434;
XX
XX 27-JAN-2005 (first entry)
XX
XX Novel [glutaminyl cyclase (QC) inhibitor-related protein #2.
XX Alzheimer's disease; Down's syndrome; Huntington's disease;
XX glutaminyl cyclase inhibitor; QC inhibitor; neurotrophic; neuroprotective;
XX anti-Parkinsonian; neuroleptic; antipyretic; antidepressant; hypotensive;
XX eating-disorders-Gen; anticonvulsant; antialcoholic; antidiabetic;
XX hypnotic; CNS-gen; endocrine-Gen; tranquiliser; antituber; cyostatic;
XX antiinflammatory; antiproliferative; antithrombotic; antihypertensive;
XX antiarteriosclerotic; pyroglyutamic acid; neuronal disease;
XX Parkinson's disease; Huntington's chorea; pathogenic psychotic condition;
XX schizophrenia; impaired food intake; sleep-wakefulness;
XX homeostatic regulation; energy metabolism; autonomic function;
XX hormonal balance; body fluid regulation; hypertension; fever;
XX sleep dysregulation; anorexia; anxiety related disorder; depression;
XX seizure; epilepsy; drug withdrawal; alcoholism;
XX neurodegenerative disorder; cognitive dysfunction; dementia; ulcer;
XX gastric cancer; neoplasia; inflammatory host response; cancer; melanoma;
XX malignant metastasis; psoriasis; rheumatoid arthritis; atherosclerosis;
XX leukocyte adhesion.
XX
XX Unidentified.
XX
XX OS
XX PN US2004224875-A1.
XX PD 11-NOV-2004.
```

PF 05-MAY-2004; 2004US-00838993.
 XX
 XX 05-MAY-2003; 2003US-0468014P.
 XX
 XX (SCHILLING S.
 PA (NIESTROJ A J.
 PA (HEISER U.
 PA (BUCH/) BUCHHOLZ M.
 PA (DEMUTH H.
 XX
 PI Schilling S, Niestroj AJ, Heiser U, Buchholz M, Demuth H;
 XX
 DR WPI; 2004-813067/80.
 XX
 PT Use of glutaminyl cyclase inhibitor for the treatment of e.g. Alzheimer's
 PT disease, Down syndrome, pathogenic psychotic conditions, schizophrenia
 PT and Huntington's disease.
 XX
 PS Disclosure; Page 5; 34pp; English.
 XX
 CC This invention relates to a novel treatment of Alzheimer's disease.
 CC Down's syndrome or Huntington's disease which involves administering a
 CC glutaminyl cyclase (QC) inhibitor. The invention may be useful for the
 CC development of compounds with a nootropic, neuroprotective,
 CC antiparkinsonian, neuroleptic, antipyretic, antidepressant, hypotensive,
 CC eating-disorders-Gen, anticonvulsant, antialcoholic, antiaddictive,
 CC hypnotic, CNS-Gen, endocrine-Gen, tranquiliser, antiulcer, cyostatic,
 CC antiinflammatory, antiporiatic, antirheumatic, antiarthritic or
 CC antiarteriosclerotic activity acting as glutaminyl cyclase inhibitors.
 CC Glutaminyl cyclase catalyzes both the intramolecular cyclisation of N-
 CC terminal glutamate residues into pyroglutamic acid with liberation of
 CC ammonia and the intramolecular cyclisation of N-terminal glutamate
 CC residues into pyroglutamic acid with liberation of water, the glutaminyl
 CC cyclase inhibitors are useful in the treatment of various neuronal
 CC diseases. The composition containing a QC inhibitor is useful for the
 CC treatment of neuronal disorders such as Alzheimer's disease, Down
 CC syndrome, Parkinson's disease, Chorea Huntington, pathogenic psychotic
 CC conditions, schizophrenia, impaired food intake, sleep-wakefulness,
 CC impaired homeostatic regulation of energy metabolism, impaired autonomic
 CC function, impaired hormonal balance, impaired regulation of body fluids,
 CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
 CC disorders (including depression), seizures including epilepsy, drug
 CC withdrawal and alcoholism), and neurodegenerative disorders (such as
 CC cognitive dysfunction and dementia). The compositions may also be useful
 CC for the treatment of ulcer, gastric cancer, neoplasia, inflammatory host
 CC responses, cancer, melanoma, malignant metastasis, psoriasis, rheumatoid
 CC arthritis, atherosclerosis and leukocyte adhesion and migration processes
 CC in the endothelium. The present sequence is that of a protein which is
 CC related to the treatment method of the invention.
 XX
 SQ Sequence 40 AA;
 OY
 DB 1 DAERFHDGVEVHHQKLVFPAEDVGSNKGA 30
 1 DAERFHDGVEVHHQKLVFPAEDVGSNKGA 30
 1 DAERFHDGVEVHHQKLVFPAEDVGSNKGA 30

RESULT 95
 ADU46708
 ID ADU46708 standard; peptide; 40 AA.
 XX
 AC ADU46708;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Amyloid beta peptide (1-40), substrate of glutaminyl cyclase.
 XX
 KW Amyloid-beta peptide (1-40); glutaminyl cyclase; nootropic;
 neuroprotective; anticonvulsant; antiulcer; cyostatic; neuroleptic;

KW antifertility; antiporiatic; antirheumatic; antiarthritic;
 KW antiarteriosclerotic; Alzheimer's disease; human.
 XX
 OS Homo sapiens.
 XX
 FN WO2004098625-A2.
 XX
 PD 18-NOV-2004.
 XX
 XX 05-MAY-2004; 2004WO-EP004778.
 XX
 XX 05-MAY-2003; 2003US-0468014P.
 PR 05-MAY-2003; 2003US-0468043P.
 PR 15-OCT-2003; 2003US-0512038P.
 XX
 PA (PROB-) PROBIODRUG AG.
 XX
 XX Demuth H, Hoffmann T, Niestroj AJ, Schilling S, Heiser U,
 PI
 DR WPI; 2004-805062/79.
 XX
 PT Use of effectors of glutaminyl cyclase (QC) for treating diseases and/or
 PT for modulating physiological processes based on the action of pglu-
 PT containing peptides.
 XX
 PS Disclosure; Page 12; 106pp; English.
 XX
 CC The present sequence is that of amyloid beta peptide (1-40).
 CC Pyroglutamate (pGlu)-containing isoforms of amyloid beta peptides
 CC represent the prominent forms of N-truncated amyloid beta peptides in
 CC senile plaques. The pGlu modification exacerbates the toxic properties of
 CC amyloid beta peptides. The invention shows that glutaminyl cyclase (QC,
 CC EC 2.3.2.5) is involved in the cyclisation of Glu to pGlu, making this
 CC enzyme a target in drug development. The invention relates to the
 CC identification, screening and use of effectors of QC for the preparation
 CC of a medicament for: (a) the treatment of diseases that can be treated by
 CC modulation of QC activity in vivo; and/or (b) the modulation of
 CC physiological processes based on the action of pglu-containing peptides
 CC caused by modulation of QC activity. The QC effectors are used to alter
 CC the conversion of N-terminal Glu or Gln residues to pglu residues in a QC
 CC substrate such as amyloid beta3-40/42. They can be used to treat
 CC Alzheimer's disease, Down Syndrome, Huntington's disease, Kennedy's
 CC disease, ulcer disease and gastric cancer with or without Helicobacter
 CC pylori infections, pathogenic psychotic conditions, schizophrenia,
 CC infertility, neoplasia, inflammatory host responses, cancer, malign
 CC metastasis, melanoma, psoriasis, rheumatoid arthritis, atherosclerosis,
 CC impaired humoral and cell-mediated immune responses, leukocyte adhesion
 CC and migration processes in the endothelium, impaired food intake, sleep-
 CC wakefulness, impaired homeostatic regulation of energy metabolism,
 CC impaired autonomic function, impaired hormonal balance and impaired
 CC regulation of body fluids. The effectors of QC are also useful for:
 CC regulating and/or controlling male fertility; stimulating
 CC gastrointestinal tract cell proliferation, preferably proliferation of
 CC gastric mucosal cells, epithelial cells, acute acid secretion and for
 CC differentiating acid-producing parietal cells and histamine-secreting
 CC enterochromaffin-like cells (all claimed). Amyloid beta peptides were
 CC also shown to be substrates of dipeptidyl peptidase IV (DP IV) and DP IV-
 CC like enzymes, and preferred effector compositions additionally comprise
 CC inhibitors of these enzymes.
 XX
 SQ Sequence 40 AA;
 OY
 DB 1 DAERFHDGVEVHHQKLVFPAEDVGSNKGA 30
 1 DAERFHDGVEVHHQKLVFPAEDVGSNKGA 30

RESULT 96
 ADV50991

ID	ADVS0091	standard; peptide; 40 AA.
XX	ADVS0091;	
XX	ADVS0091;	
XX	ADVS0091;	
DT	10-MAR-2005	(first entry)
XX	Alzheimers disease-related beta amyloid 40 peptide.	
DE	Alzheimers disease-related beta amyloid 40 peptide.	
XX	Beta amyloid; neuroprotective; nootropic; Alzheimers disease;	
KM	degeneration; neurological disease.	
XX	Unidentified.	
OS	Unidentified.	
XX	JP2004361227-A.	
PN	24-DEC-2004.	
PD	24-DEC-2004.	
XX	04-JUN-2003; 2003JP-00159562.	
PF	04-JUN-2003; 2003JP-00159562.	
XX	04-JUN-2003; 2003JP-00159562.	
PR	04-JUN-2003; 2003JP-00159562.	
XX	(KOKU-) KOKURITSU DAIGAKU HOJIN TOHOKU DAIGAKU.	
PA	(KOKU-) KOKURITSU DAIGAKU HOJIN TOHOKU DAIGAKU.	
XX	WPI; 2005-044038/05.	
DR	WPI; 2005-044038/05.	
XX	Comprehensive identification of beta amyloid binding protein expressed in	
PT	brain, for use against Alzheimer's disease, comprises performing a	
PT	proteomic technique.	
XX	proteomic technique.	
XX	Example; Page; 26pp; Japanese.	
PS	Example; Page; 26pp; Japanese.	
XX	The invention relates to a novel method for comprehensive identification	
CC	of a beta amyloid-binding protein, which is expressed in the brain and	
CC	has a capacity to bind with beta amyloid 40. The method comprises	
CC	performing a proteomic technique. The method of the invention	
CC	neuroprotective and nootropic applications. The method of the invention	
CC	may be useful in screening for a compound which inhibits the interaction	
CC	between beta amyloid and a beta amyloid-binding protein. The beta amyloid	
CC	-binding protein may be useful as an effective agent against Alzheimers	
CC	disease. The current sequence is that of the beta amyloid 40 peptide of	
CC	the invention.	
XX	the invention.	
SQ	Sequence 40 AA;	
XX	Sequence 40 AA;	
Query Match	100.0%; Score 162; DB 9; Length 40;	
Best Local Similarity	100.0%; Pred. No. 7.9e-18;	
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGK 30	
DB	1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGK 30	
RESULT 97		
ID	ADM38388	standard; peptide; 40 AA.
XX	ADM38388	
AC	ADM38388;	
XX	ADM38388;	
DT	07-APR-2005	(first entry)
XX	Human beta amyloid peptide, seqid:1.	
DE	Human beta amyloid peptide, seqid:1.	
XX	Amyloid; antiagregant; beta-amyloid.	
KM	Amyloid; antiagregant; beta-amyloid.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	US2005009749-A1.	
PN	13-JAN-2005.	
PD	13-JAN-2005.	
XX	02-JUL-2004; 2004US-00884729.	
PF	02-JUL-2004; 2004US-00884729.	
XX	02-JUL-2004; 2004US-00884729.	

PR	11-JUL-2003; 2003KR-00047199.
XX	
PA	(AHN//) AHN J. S.
PA	(JOI//) JO I.
PA	(KMOM//) KMOM H. J.
PA	(KIMC//) KIM C. J.
PA	(PARK//) PARK J. E.
PI	Ahn JS, Jo I, Kwon HT, Kim CJ, Park JE;
XX	
DR	WPI: 2005-074526/08.
XX	
PT	New beta-amyloid aggregation inhibiting protein, useful for treating
PT	neurodegenerative disorders, such as Alzheimer's disease or Down's
PT	Syndrome.
XX	
PS	Disclosure; SEQ ID NO 1; 19pp; English.
XX	
CC	The present invention relates to the Streptomyces sp. beta-amyloid
CC	aggregation inhibiting protein and its encoding DNA. The invention is
CC	useful in treating neurodegenerative disorders, such as Alzheimer's
CC	disease or Down's Syndrome. The present sequence is the human beta
CC	amyloid peptide.
XX	
XX	Sequence 40 AA;
XX	
XX	Query Match 100.0%; Score 162; DB 9; Length 40;
XX	Best Local Similarity 100.0%; Pred. No. 7.9e-18;
XX	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 DAERFHDGCVHHQKLVFFAEDVGSNKGCA 30
DB	1 DAERFHDGCVHHQKLVFFAEDVGSNKGCA 30
XX	
XX	RESULT 98
XX	ADY72249
XX	ID ADY72249 standard; protein; 40 AA.
AC	ADY72249;
XX	
DT	02-JUN-2005 (first entry)
XX	
DE	N-terminal amyloid beta protein (1-40) Seq 16.
XX	
KW	amyloid; Alzheimers disease; Parkinsons disease; prion infection; BSE;
XX	Creutzfeldt Jakob disease; antiparkinsonian; neuroprotective; nootropic;
KW	cerebroprotective.
XX	
OS	Unidentified.
XX	
PH	Key Location/Qualifiers
FT	Modified-site 1
FT	/note= "N-terminal acetyl"
XX	
PN	JP2005065660-A.
XX	
PD	17-MAR-2005.
XX	
PF	28-AUG-2003; 2003JP-00304195.
XX	
PR	28-AUG-2003; 2003JP-00304195.
XX	
PA	(RIKO-) ZH RIKOGAKU SHINKOKAI.
XX	
DR	WPI: 2005-218302/23.
XX	
PT	RNA aptamers capable of inhibiting amyloid fiber formation, useful for
PT	treating or preventing disease caused by accumulation, production or
PT	proliferation of amyloid fibers such as Alzheimer's disease and
PT	Parkinson's disease.
XX	
XX	Disclosure; SEQ ID NO 16; 11pp; Japanese.

XX This invention relates to RNA molecules that are capable of inhibiting
CC amyloid fiber formation. Specifically, it refers to any one of 15 fully
CC defined 88, 89 or 90 RNA nucleotide aptamers given in the specification
CC or sequence variants thereof. The present invention describes DNA oligos
CC having a base sequence complementary to the base sequence of the RNA
CC oligos, vectors comprising such DNA oligos and pharmaceutical
CC compositions containing the RNA aptamers or the vectors aforementioned.
CC Accordingly, the RNA aptamers or encoding vectors are useful for treating
CC or preventing a disease caused by the accumulation, production or
CC proliferation of amyloid fiber including Alzheimer's disease, Parkinson's
CC disease and prion diseases such as BSE and Creutzfeldt Jakob disease.
CC Furthermore, these pharmaceutical compositions exhibit antiparkinsonian,
CC neuroprotective, neurotropic and cerebroprotective activities. This
CC polypeptide sequence is the N-terminal amyloid beta protein (1-40) of the
CC invention.
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 99
ADY81764
ID ADY81764 standard; peptide; 40 AA.
XX
AC ADY81764;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human beta-amyloid residues 1-40.
XX
KW cerebroprotective; neurotropic; neuroprotective; diagnostic; immunotherapy;
KW Alzheimer's disease; degeneration; neurological disease;
KW cognitive disorder; beta-amyloid; amyloid protein.
XX
OS Homo sapiens.
XX
PN WO2005025616-A1.
XX
PD 24-MAR-2005.
XX
PE 08-SEP-2004; 2004WO-JP013397.
XX
PR 09-SEP-2003; 2003JP-00317443.
XX
PA (TAKE) TAKEDA PHARM CO LTD.
XX
PI Shoji M, Asami A, Suzuki N;
XX
DR WPI; 2005-242286/25.
XX
PT Preventive and therapeutic agent useful for treating and preventing
PT Alzheimer's disease, mild cognitive impairment, or brain amyloid
PT angiopathy, comprises antibody capable of reacting with partial peptide
PT in C-terminal of beta-amyloid.
XX
PS Claim 5; SEQ ID NO 3; 44pp; Japanese.
XX
XX The invention describes a preventive and therapeutic agent (I) of an
CC Alzheimer's disease, mild cognitive impairment or brain amyloid
CC angiopathy, comprising a monoclonal antibody (A1) reacting specifically
CC with a partial peptide in the C terminal of beta-amyloid or its
CC derivative(s), where A1 does not recognize the partial peptide of beta-
CC amyloid comprising a 11 amino acid sequence (SEQ ID No. 8) fully defined
CC in the specification. (A1) is useful for manufacturing the preventive-
CC therapeutic agent (I) which is administered in order to prevent and treat

CC Alzheimer's disease, mild cognitive impairment or brain amyloid
CC angiopathy. (I) is useful as diagnostic agent for Alzheimer's disease.
CC (I) is capable of removing beta-amyloid from a formed senile plaque. (I)
CC inhibits aggregation of beta-amyloid in the brain. (I) arrests beta-
CC amyloid at the periphery region. (I) does not induce bleeding from the
CC cerebral blood vessel. This is the amino acid sequence of human beta-
CC amyloid residues 1-38.
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 162; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.9e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 100
ADY78385
ID ADY78385 standard; peptide; 40 AA.
XX
AC ADY78385;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human amyloid peptide A40.
XX
KW Monoclonal antibody; vaccine; amyloid protein; diagnosis;
KW Alzheimer's disease; neuroprotective; neurotropic; degeneration;
KW neurological disease; amyloidosis; metabolic disorder; multiple myeloma;
KW cytosarctic; hematological disease; immune disorder; BSE; infection;
KW scrapie; parkinson's disease; antiparkinsonian; Huntingtons chorea;
KW anticonvulsant; genetic disorder; motor neuron disease; cms-gen.;
KW muscular-gen.; Creutzfeldt Jakob disease; kuru;
KW non-insulin dependent diabetes; antidiabetic; endocrine disease;
KW gastrointestinal disease; macular degeneration; ophthalmological;
KW ocular disease; epilothe.
XX
OS Homo sapiens.
XX
PN WO2005025616-A2.
XX
PD 24-MAR-2005.
XX
PE 13-SEP-2004; 2004WO-US029946.
XX
PR 12-SEP-2003; 2003US-0502326P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Glabe CG, Kaye R;
XX
DR WPI; 2005-233409/24.
XX
PT New composition with isolated monoclonal antibodies binding a
PT conformational epitope of a prefibrillar aggregate contributing to
PT amyloid fibril formation, useful in diagnosing or treating Alzheimer's
PT disease or other amyloid diseases.
XX
PS Disclosure; SEQ ID NO 1; 39pp; English.
XX
XX The invention relates to a composition comprising an isolated monoclonal
CC antibody which binds to a conformational epitope of a prefibrillar
CC aggregate which forms in a human or animal contributing to amyloid fibril
CC formation, the monoclonal antibody being specific for a conformation-
CC dependent epitope that is preferentially displayed by oligomeric
CC conformations of A-beta and other amyloids. Also included are a
CC preparation comprising at least one monoclonal antibody cited in the
CC composition cited above in combination with at least one anti-
CC inflammatory agent, a composition (comprising a monoclonal antibody which
CC binds to an epitope of a prefibrillar aggregate which forms in a human or

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OM protein - protein search, using sw model

Run on: April 20, 2006, 10:05:26 ; Search time 47 seconds
(without alignments)
52.772 Million cell updates/sec

Title: US-10-666-423-1
Perfect score: 162
Sequence: 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	162	100.0	30	2	US-09-861-847A-1
3	162	100.0	33	1	US-08-609-090-4
4	162	100.0	35	1	US-08-304-585-6
5	162	100.0	36	1	US-08-609-090-6
6	162	100.0	36	2	US-09-861-847A-6
7	162	100.0	36	2	US-09-861-847A-11
8	162	100.0	38	1	US-08-302-808-1
9	162	100.0	38	1	US-07-737-371E-68
10	162	100.0	38	1	US-08-986-948-1
11	162	100.0	38	2	US-09-623-548A-975
12	162	100.0	38	2	US-09-623-548A-1002
13	162	100.0	38	2	US-09-657-276-975
14	162	100.0	38	2	US-09-657-276-1002
15	162	100.0	39	1	US-08-302-808-2
16	162	100.0	39	1	US-08-609-090-7
17	162	100.0	39	1	US-08-682-245A-1
18	162	100.0	39	1	US-08-986-948-2
19	162	100.0	40	1	US-07-744-767A-1
20	162	100.0	40	1	US-08-235-400-2
21	162	100.0	40	1	US-08-476-464A-2
22	162	100.0	40	1	US-08-304-585-1
23	162	100.0	40	1	US-08-302-808-3
24	162	100.0	40	1	US-08-433-734-1
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26	162	100.0	40	1	US-07-737-371E-69
27	162	100.0	40	1	US-08-682-245A-2

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53	162	100.0	42	1	US-07-744-767A-2	Sequence 2, Appli
54	162	100.0	42	1	US-08-179-574-1	Sequence 1, Appli
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57	162	100.0	42	1	US-08-123-659A-19	Sequence 19, Appli
58	162	100.0	42	1	US-08-464-247A-19	Sequence 19, Appli
59	162	100.0	42	1	US-08-464-248A-19	Sequence 19, Appli
60	162	100.0	42	1	US-08-476-464A-1	Sequence 1, Appli
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62	162	100.0	42	1	US-08-302-808-5	Sequence 5, Appli
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ALIGNMENTS

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RESULT 1
US-08-609-090-3
; Sequence 3, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-3

Query Match          100.0%; Score 162; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGA 30

RESULT 2
US-09-661-847A-1
; Sequence 1, Application US/09861847A
; Patent No. 6713450
; GENERAL INFORMATION:
; APPLICANT: FRANGIONE, Bias
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: SIGURSSON, Einar
; TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDGENIC PEPTIDES
; TITLE OF INVENTION: HOMOLOGOUS TO AMYLOID BETA FOR INDUCTION OF AN IMMUNE
; TITLE OF INVENTION: RESPONSE TO AMYLOID BETA AND AMYLOID DEPOSITS
; FILE REFERENCE: 5986/1K43-US1
; CURRENT APPLICATION NUMBER: US/09/861,847A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/016,233
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; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRP
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-861-847A-1
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DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGA 30
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RESULT 3
US-08-609-090-4
; Sequence 4, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-4
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Best Local Similarity 100.0%; Pred. No. 6.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGA 30
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RESULT 4
US-08-304-585-6
Sequence 6, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: MAGGIO, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueiting, Raach, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueiting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-6
Query Match 100.0%; Score 162; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 7,4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 5
US-08-609-090-6
Sequence 6, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPETIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-6
Query Match 100.0%; Score 162; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
RESULT 6
US-09-861-847A-6
Sequence 6, Application US/09861847A
Patent No. 6713450
GENERAL INFORMATION:
APPLICANT: FRANGIONE, Blas
APPLICANT: MISNIEMSKI, Thomas
APPLICANT: SIGURDSSON, Rinar
TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDOGENIC PEPTIDES
TITLE OF INVENTION: HOMOLOGOUS TO AMYLOID BETA FOR INDUCTION OF AN IMMUNE
FILE REFERENCE: 5986/1K433-US1
CURRENT APPLICATION NUMBER: US/09/861,847A
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/016,233
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 36
TYPE: PPT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: C-terminal residue 36 may be amidated.
US-09-861-847A-6
Query Match 100.0%; Score 162; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 36
RESULT 7
US-09-861-847A-11
Sequence 11, Application US/09861847A
Patent No. 6713450

GENERAL INFORMATION:
APPLICANT: FRANGIONE, Blas
APPLICANT: WISNIEMSKI, Thomas
APPLICANT: SIGURDSSON, Einar
TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDGENIC PEPTIDES
TITLE OF INVENTION: HOMOLOGOUS TO AMYLOID BETA FOR INDUCTION OF AN IMMUNE
TITLE OF INVENTION: RESPONSE TO AMYLOID BETA AND AMYLOID DEPOSITS
FILE REFERENCE: 5986/1K433-US1
CURRENT FILING DATE: 2001-05-22
PRIORITY FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 11
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
US-09-861-847A-11

Query Match 100.0%; Score 162; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30

RESULT 8
US-08-302-808-1
Sequence 1, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uh1ro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J994/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-1

Query Match 100.0%; Score 162; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 8,2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30

RESULT 9
US-07-737-371E-68
Sequence 68, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yantner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-68
Query Match 100.0%; Score 162; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 8,2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 10

US-08-986-948-1
; Sequence 1, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uh1ro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chioko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-986-948-1

Query Match 100.0%; Score 162; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 11

US-09-623-548A-975
; Sequence 975, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 975
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-623-548A-975

Query Match 100.0%; Score 162; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 12

US-09-623-548A-1002
; Sequence 1002, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1002
; LENGTH: 38

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1002
Query Match      100.0%; Score 162; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGK 30
DB      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGK 30

RESULT 13
US-09-657-276-975
; Sequence 975; Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 975
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-975
Query Match      100.0%; Score 162; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGK 30
DB      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGK 30

RESULT 14
US-09-657-276-1002
; Sequence 1002; Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
```

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; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1002
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1002
Query Match      100.0%; Score 162; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGK 30
DB      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGK 30

RESULT 15
US-08-302-808-2
; Sequence 2; Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
```


TELEFAX: 617-523-6440
TELEX: 200291 STRB
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-2

Query Match 100.0%; Score 162; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 16
US-08-609-090-7
Sequence 7, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-7

Query Match 100.0%; Score 162; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 17
US-08-682-245A-1
Sequence 1, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHERALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NOBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-1

Query Match 100.0%; Score 162; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 18
US-08-986-948-2
Sequence 2, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRP
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-2

Query Match 100.0%; Score 162; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGA 30

RESULT 19
US-07-744-767A-1
Sequence 1, Application US/07744767A
Patent No. 5434050
GENERAL INFORMATION:
APPLICANT: Magglo, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN

COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,767A
FILING DATE: 13-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600,226-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0311
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-744-767A-1

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGA 30

RESULT 20
US-08-235-400-2
Sequence 2, Application US/08235400
Patent No. 5552426
GENERAL INFORMATION:
APPLICANT: Lunn, William H.
APPLICANT: Morn, James A.
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,400
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-400-2

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 21
US-08-476-464A-2

Sequence 2, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-2

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 22
US-08-304-585-1

Sequence 1, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND

TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeling, Raach, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA

ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.

REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-1

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 23
US-08-302-808-3

Sequence 3, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349unhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-3

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 24
US-08-433-734-1
Sequence 1, Application US/08433734
Patent No. 5897472
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantyla, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: For Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muelting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1226
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-1

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 25
US-08-609-090-8
Sequence 8, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1124
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-8

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 26
US-07-737-371E-69
Sequence 69, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-69

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 27
US-08-682-245A-2
Sequence 2, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEPALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHARABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-2

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 28
US-08-986-948-3
Sequence 3, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhix
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:

Wed May 10 11:59:10 2006

us-10-666-423-1.top100.ra1

Page 12

NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEFAX: 200281-STRB
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-3

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30

RESULT 29
US-08-461-216-1
Sequence 1, Application US/08461216
Patent No. 5958883
GENERAL INFORMATION:
APPLICANT: SNOW, A.D.
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,734
FILING DATE: October 23, 1992
APPLICATION NUMBER: 07/950,417
FILING DATE: September 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: UOFW-1-6707
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
TELEFAX: 1-206-224-0779
TELEFAX: 4938023
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide

DESCRIPTION: {SYMBOL 98 \F "Symbol"/A4(1-40);
FIGURES 23-29
US-08-461-216-1

Query Match 100.0%; Score 162; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30

RESULT 30
US-08-959-148-1
Sequence 1, Application US/08959148
Patent No. 6172277
GENERAL INFORMATION:
APPLICANT: Tate, Barbara A.
APPLICANT: Newton, Julie L.
TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
FILE REFERENCE: 04930/022001
CURRENT APPLICATION NUMBER: US/08/959,148
CURRENT FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-08-959-148-1

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30

RESULT 31
US-09-242-724-22
Sequence 22, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-09-242-724-22

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKG 30

RESULT 32
US-08-723-661B-1
Sequence 1, Application US/08723661B

US-09-861-847A-7

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 11 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 40

RESULT 36

US-09-861-847A-8
Sequence 8, Application US/09861847A
Patent No. 6713450
GENERAL INFORMATION:
APPLICANT: FRANGIONE, Blas
APPLICANT: WISNIEWSKI, Thomas
APPLICANT: SIGURDSSON, Einar
TITLE OF INVENTION: SYNTHETIC IMMUNOGENIC BUT NON-AMYLOIDGENIC PEPTIDES
TITLE OF INVENTION: HOMOLOGOUS TO AMYLOID BETA FOR INDUCTION OF AN IMMUNE
TITLE OF INVENTION: RESPONSE TO AMYLOID BETA AND AMYLOID DEPOSITS
FILE REFERENCE: 5986/1K433-US1
CURRENT APPLICATION NUMBER: US/09/861,847A
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/016,233
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: misc feature
OTHER INFORMATION: Amino acid residues 35-40 can either be absent or present as Lys
OTHER INFORMATION: or Asp to form, in combination with residues 31-34, a C-terminal
OTHER INFORMATION: polylysine or polyaaspartate segment of 4-10 residues in length
US-09-861-847A-8

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 37
US-09-988-842-3
Sequence 3, Application US/09988842
Patent No. 6716589
GENERAL INFORMATION:
APPLICANT: Johansson, Jan
TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
FILE REFERENCE: 12125-002001
CURRENT APPLICATION NUMBER: US/09/988,842
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US 60/251,662
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 60/253,695
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetically generated peptide

US-09-988-842-3

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 38

US-10-455-218-1
Sequence 1, Application US/10455218
Patent No. 6770448
GENERAL INFORMATION:
APPLICANT: Glabe, Charles
APPLICANT: Garzon-Rodriguez, William
TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 50016/002002
CURRENT APPLICATION NUMBER: US/10/455,218
CURRENT FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US/09/133,866
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-455-218-1

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 39
US-10-151-614-1
Sequence 1, Application US/10151614
Patent No. 6821504
GENERAL INFORMATION:
APPLICANT: WISNIEWSKI, Thomas
APPLICANT: TURNBULL, Daniel
APPLICANT: SIGURDSSON, Einar
APPLICANT: ZAIM WADGHIRI, Yousssef
TITLE OF INVENTION: DETECTION OF ALZHEIMER'S AMYLOID BY MAGNETIC RESONANCE
FILE REFERENCE: WISNIEWSKI 2A
CURRENT APPLICATION NUMBER: US/10/151,614
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/292,625
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-614-1

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 40

US-09-623-548A-956
; Sequence 956, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 956
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-956

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 41

US-09-623-548A-978
; Sequence 978, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 978

; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-978

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 42

US-09-623-548A-989
; Sequence 989, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 989
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-989

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 43

US-09-623-548A-1005
; Sequence 1005, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

```

; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1005
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1005

Query Match          100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30

RESULT 44
US-09-657-276-956
; Sequence 956, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 956
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-956

Query Match          100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30

Query Match          100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
```

```

RESULT 45
US-09-657-276-978
; Sequence 978, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 978
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-978

Query Match          100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8,7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGA 30

RESULT 46
US-09-657-276-989
; Sequence 989, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 989
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-657-276-989

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30

RESULT 47
US-09-657-276-1005
Sequence 1005; Application US/09657276

GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONFIGURATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1005
LENGTH: 40
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-1005

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30

RESULT 48
US-09-962-955D-36
Sequence 36; Application US/09962955D
Patent No. 6933280
GENERAL INFORMATION:
APPLICANT: CASTILLO, GERARDO
APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
FILE REFERENCE: PROTEO.P03CI
CURRENT APPLICATION NUMBER: US/09/962,955D
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/938,275
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/947,057
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: 60/027,981

PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 36

LENGTH: 40
TYPE: PPT
ORGANISM: Mus musculus
US-09-962-955D-36

Query Match 100.0%; Score 162; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30

RESULT 49
PCT-US92-06700-1
Sequence 1; Application PC/TUS9206700

GENERAL INFORMATION:
APPLICANT: Manlyh, Patrick W.
APPLICANT: Maggio, John E.
TITLE OF INVENTION: Labelled -Amyloid Peptide
TITLE OF INVENTION: and Alzheimer's Disease Detection
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 3100 Northwest Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: Northgate 386
OPERATING SYSTEM: DOS 4.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06700
FILING DATE: 19920810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.226-WO-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
FEATURE:
NAME/KEY: Internal fragment of the -
NAME/KEY: amyloid peptide precursor
LOCATION: Represents isolated internal
LOCATION: sequence of 40 amino acid residues from
LOCATION: the -amyloid peptide precursor
PCT-US92-06700-1

Query Match 100.0%; Score 162; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.7e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30

```
RESULT 50
US-08-302-808-4
; Sequence 4, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhitro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-4

Query Match 100.0%; Score 162; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30
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RESULT 51
US-08-682-245A-3
; Sequence 3, Application US/08682245A
```

```
; Patent No. 5919631
; GENERAL INFORMATION:
; APPLICANT: GOYAL, SHEPALI
; APPLICANT: PAUL, JOSEPH M
; APPLICANT: RIEDEL, ROBERT G
; APPLICANT: SARASRABUDHE, SUDHIR
; TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
; AGGREGATION OF THE B44 PEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOECHST MARION ROUSSEL, INC.
; STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
; CITY: CINCINNATI
; STATE: OHIO
; COUNTRY: U.S.A.
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,245A
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,414
; FILING DATE: 16-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LENTZ, NELSEN L
; REGISTRATION NUMBER: 38,537
; REFERENCE/DOCKET NUMBER: HR-1257A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-7369
; TELEFAX: 513-948-7961 OR 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-682-245A-3

Query Match 100.0%; Score 162; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30

RESULT 52
US-08-986-948-4
; Sequence 4, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uhitro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
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```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELETYPE: 200291 STRE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-986-948-4

Query Match 100.0%; Score 162; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 53
US-07-744-767A-2
; Sequence 2, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Magglio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: -Amyloid Peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600,226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-744-767A-2

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 54
US-08-179-574-1
; Sequence 1, Application US/08179574
; Patent No. 5506097
; GENERAL INFORMATION:
; APPLICANT: Huntington Potter
; APPLICANT: Usamah Kayyali
; TITLE OF INVENTION: Compounds and Methods for Inhibiting
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/819,361
; FILING DATE: 13-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: H090-03A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-179-574-1

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 55

US-08-347-144-1
Sequence 1, Application US/08347144
Patent No. 5589154
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,144
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: B-Amyloid Peptide
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 56
US-08-462-859A-19
Sequence 19, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne

STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3305
TELEFAX: (201)831-3246
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-19

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 57
US-08-123-659A-19
Sequence 19, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosebldum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosebldum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-19

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 58
US-08-464-247A-19
Sequence 19, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
ATTORNEY/AGENT INFORMATION:
VITEK, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-19
Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 59
US-08-464-248A-19
Sequence 19, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.

APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 831-3246
TELEFAX: (201) 831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 60
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
ATTORNEY/AGENT INFORMATION:
DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-2400
TELEFAX: (415)576-0300 1:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
DB 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 61
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantlyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 561415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muelting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULAR TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
DB 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 62
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, ARIKO
APPLICANT: KITAHARA, CHIEKO
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 15-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-5

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
DB 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 63
US-08-268-348A-1
Sequence 1, Application US/08268348A


```
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobeli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotteman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-1

Query Match      100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
DB      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 64
US-08-268-348A-3
Sequence 3, Application US/08268348A
GENERAL INFORMATION:
APPLICANT: Dobeli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotteman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
```

```
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-3

Query Match      100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
DB      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 65
US-08-268-348A-4
Sequence 4, Application US/08268348A
GENERAL INFORMATION:
APPLICANT: Dobeli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotteman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-4

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

RESULT 66
US-08-268-348A-5
Sequence 5, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobelli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-5

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

RESULT 67
US-08-268-348A-6
Sequence 6, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobelli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-6

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

RESULT 68
US-08-433-734-2
Sequence 2, Application US/08433734
Patent No. 5837473
GENERAL INFORMATION:

APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: for use in detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueiting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-2

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 69
US-08-609-090-9
Sequence 9, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-9

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30

RESULT 70
US-07-737-371E-72
Sequence 72, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-72

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed May 10 11:59:10 2006

us-10-666-423-1.top100.ra

Page 26

Qy 1 DAEPHDSGYEVHHQKLVFPAEDVGSNKGA 30
|||||
Db 1 DAEPHDSGYEVHHQKLVFPAEDVGSNKGA 30

RESULT 71
 US-08-422-333--4
 ; Sequence 4, Application US/08422333
 ; Patent No. 5912410
 ; GENERAL INFORMATION:
 APPLICANT: CORDELL, Barbara L.
 TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
 TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scios, Inc.
 STREET: 2450 Bayshore Parkway
 CITY: Mountain View
 STATE: CA
 COUNTRY: USA
 ZIP: 94043
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/422,333
 FILING DATE: 13-APR-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Shearer, Peter R.
 REGISTRATION NUMBER: 28,117
 REFERENCE/DOCKET NUMBER: 21900-28048.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 966-1550
 TELEFAX: (415) 968-2458
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

RESULT 72
US-08-682-245A-4
Sequence 4, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOTAL, SHERALI
APPLICANT: PAUL, JOSEPH M
APPLICANT: RIDEHL, NOBERT G
APPLICANT: SARASRABUHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300

```

1      COMPUTER READABLE FORM:
2      MEDIUM TYPE: Floppy disk
3      COMPUTER: IBM PC compatible
4      OPERATING SYSTEM: PC-DOS/MS-DOS
5      SOFTWARE: Patent In Release #1.0, Version #1.10
6      CURRENT APPLICATION DATA:
7      APPLICATION NUMBER: US/08/682,245A
8      FILING DATE: 17-JUN-1996
9      CLASSIFICATION: 435
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: US 60/039,414
12     FILING DATE: 16-AUG-1995
13     ATTORNEY/AGENT INFORMATION:
14     NAME: LENTZ, NELSEN L
15     REGISTRATION NUMBER: 38,537
16     REFERENCE/DOCKET NUMBER: HR-1257A
17     TELECOMMUNICATION INFORMATION:
18     TELEPHONE: 513-948-7369
19     TELEFAX: 513-948-7961 OR 4681
20     TELEX: 214320
21     INFORMATION FOR SEQ ID NO: 4:
22     SEQUENCE CHARACTERISTICS:
23     LENGTH: 42 amino acids
24     TYPE: amino acid
25     STRANDEDNESS:
26     TOPOLOGY: linear
27     MOLECULE TYPE: protein
28     US-08-682-245A-4

```

RESULT 73 948-5
 Sequence 5, Application US/08986548
 Patent No. 5255317
 GENERAL INFORMATION:
 APPLICANT: SUZUKI, No. 5955317uhiro
 APPLICANT: OKADA, Asano
 APPLICANT: KITADA, Chieko
 TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
 DERIVATIVES AND USE THEREOF
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 110 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02019
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FaalSEO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/986,948
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/302,808
 FILING DATE: 15-SEP-1994
 APPLICATION NUMBER: PCT/JP94/00089
 FILING DATE: 24-JAN-1994
 APPLICATION NUMBER: 010132/1993
 FILING DATE: 25-JAN-1993
 APPLICATION NUMBER: 019035/1993

;; FILING DATE: 05-FEB-1993
;; APPLICATION NUMBER: 286985/1993
;; FILING DATE: 16-NOV-1993
;; APPLICATION NUMBER: 334773/1993
;; FILING DATE: 28-DEC-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DAVID, RESNICK S
;; REGISTRATION NUMBER: 34,235
;; REFERENCE/DOCKET NUMBER: 44631
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-523-3400
;; TELEFAX: 617-523-6440
;; TELE: 200291 STRE
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
US-08-986-948-5

Query Match 100.0%; Score 162; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30

RESULT 74
US-08-717-551A-2
; Sequence 2, Application US/08717551A
; Patent No. 6071493
; GENERAL INFORMATION:
; APPLICANT: Dana Giullian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESS: 6 No. 60714931st LLE
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,551A
; FILING DATE: Sept-20-96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Loti Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 42 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-717-551A-2

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30

RESULT 75
US-09-388-890-1
; Sequence 1, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUBERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: AMYLOID PEPTIDE
US-09-388-890-1

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGCA 30

RESULT 76
US-09-005-215-20
; Sequence 20, Application US/09005215

```
/ Patent No. 6172043
/ GENERAL INFORMATION:
/ APPLICANT: Ingram, Vernon M.
/ APPLICANT: Blanchard, Barbara J.
/ TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
/ TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
/ STREET: 600 ATLANTIC AVENUE
/ CITY: BOSTON
/ STATE: MASSACHUSETTS
/ COUNTRY: UNITED STATES OF AMERICA
/ ZIP: 02210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/005,215
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/035,847
/ FILING DATE: 10-JAN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/960,188
/ FILING DATE: 29-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gates, Edward R.
/ REGISTRATION NUMBER: 31,616
/ REFERENCE/DOCKET NUMBER: M0656/7035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 42 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULAR TYPE: peptide
/ HYPOTHEICAL: NO
/ US-09-005-215-20

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 77
US-09-242-724-23
/ Sequence 23, Application US/09242724
/ Patent No. 6316405
/ GENERAL INFORMATION:
/ APPLICANT: Solomon, Michael E.
/ APPLICANT: Rich, Daniel H.
/ TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
/ FILE REFERENCE: Cyclosporin Analogs
/ CURRENT APPLICATION NUMBER: US/09/242,724
/ CURRENT FILING DATE: 1999-02-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO: 23
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-242-724-23
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Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 78
US-08-922-930-2
/ Sequence 2, Application US/08922930
/ Patent No. 6451544
/ GENERAL INFORMATION:
/ APPLICANT: Dana Guillan
/ TITLE OF INVENTION: Identification of Agents that Protect
/ TITLE OF INVENTION: Against Inflammatory Injury to Neurons
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
/ ADDRESSEE: & No. 6451544ris LLP
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WORDPERFECT for WINDOWS 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/922,930
/ FILING DATE: Sept-03-97
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lott, Y. Bardehl
/ REGISTRATION NUMBER: 34,293
/ REFERENCE/DOCKET NUMBER: BYLR-0039
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 42 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULAR TYPE: peptide
/ US-08-922-930-2

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGA 30

RESULT 79
US-09-660-954-1
/ Sequence 1, Application US/09660954
/ Patent No. 6471960
/ GENERAL INFORMATION:
/ APPLICANT: ANDERSON, STEPHEN
/ TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
/ OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
```

ADDRESSEE: HOWREY & SIMON
STREET: 1239 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/660,954
FILING DATE: 13-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/686,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-660-954-1
Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEPFHDSGYEVHQQKLVFPAEDVGSNKGKGA 30
DB 1 DAEPFHDSGYEVHQQKLVFPAEDVGSNKGKGA 30

RESULT 80
US-08-923-055-2
Sequence 2, Application US/08923055
Patent No. 6475742
GENERAL INFORMATION:
APPLICANT: Dana Giullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESS: & No. 6475742ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,055
FILING DATE: Sept-03-97

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-923-055-2
Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEPFHDSGYEVHQQKLVFPAEDVGSNKGKGA 30
DB 1 DAEPFHDSGYEVHQQKLVFPAEDVGSNKGKGA 30

RESULT 81
US-08-922-889-2
Sequence 2, Application US/08922889
Patent No. 6475745
GENERAL INFORMATION:
APPLICANT: Dana Giullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESS: & No. 6475745ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,889
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-922-889-2
Query Match 100.0%; Score 162; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

RESULT 82

US-09-731-460-1
; Sequence 1, Application US/09731460
; Patent No. 6495335
; GENERAL INFORMATION:
; APPLICANT: Choixier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOIXIER-04302
; CURRENT APPLICATION NUMBER: US/09/731,460
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-731-460-1

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

RESULT 83

US-09-133-866-2
; Sequence 2, Application US/09133866
; Patent No. 660017
; GENERAL INFORMATION:
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/09/133,866
; EARLIER FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: 60/055,660
; EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-133-866-2

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

RESULT 84

US-09-723-384-1
; Sequence 1, Application US/09723384

; Patent No. 6710226
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neurilab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-00474005
; CURRENT APPLICATION NUMBER: US/09/723,384
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-723-384-1

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30

RESULT 85

US-09-724-961-42
; Sequence 42, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-0047501C
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-961-42

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKA 30


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RESULT 86
; US-09-724-552-1
; Sequence 1, Application US/09724552
; Patent No. 6750324
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-00474US
; CURRENT APPLICATION NUMBER: US/09/724,552
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,019A
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/322,289
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
; US-09-724-552-1

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 87
; US-09-580-018-42
; Sequence 42, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
; US-09-580-018-42

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 88
; US-10-455-218-2
; Sequence 2, Application US/10455218
; Patent No. 6770448
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
```

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; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/10/455,218
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US/09/133,866
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-455-218-2

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 89
; US-09-723-927-1
; Sequence 1, Application US/09723927
; Patent No. 6787138
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,927
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
; US-09-723-927-1

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 90
; US-09-724-489-1
; Sequence 1, Application US/09724489
; Patent No. 6787140
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,489
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us-10-666-423-1.top100.ra1

Page 32

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/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/201,430
/ PRIOR FILING DATE: 1998-11-30
/ PRIOR APPLICATION NUMBER: US 60/067,740
/ PRIOR FILING DATE: 1997-12-02
/ PRIOR APPLICATION NUMBER: US 60/080,970
/ PRIOR FILING DATE: 1998-04-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-489-1
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
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RESULT 91
US-09-724-477-1
/ Sequence 1, Application US/09724477
/ Patent No. 6787143
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 15270J-004720US
/ CURRENT APPLICATION NUMBER: US/09/724,477
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/201,430
/ PRIOR FILING DATE: 1998-11-30
/ PRIOR APPLICATION NUMBER: US 60/067,740
/ PRIOR FILING DATE: 1997-12-02
/ PRIOR APPLICATION NUMBER: US 60/080,970
/ PRIOR FILING DATE: 1998-04-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-477-1
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
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RESULT 92
US-09-723-762-1
/ Sequence 1, Application US/09723762
/ Patent No. 6787144
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 15270J-004720US
/ CURRENT APPLICATION NUMBER: US/09/723,762
/ PRIOR FILING DATE: 2000-11-28
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/ PRIOR APPLICATION NUMBER: US/09/201,430
/ PRIOR FILING DATE: 1998-11-30
/ PRIOR APPLICATION NUMBER: US 60/067,740
/ PRIOR FILING DATE: 1997-12-02
/ PRIOR APPLICATION NUMBER: US 60/080,970
/ PRIOR FILING DATE: 1998-04-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-723-762-1
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
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RESULT 93
US-09-201-430-1
/ Sequence 1, Application US/09201430
/ Patent No. 6787529
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 15270J-004720US
/ CURRENT APPLICATION NUMBER: US/09/201,430
/ PRIOR FILING DATE: 1998-11-30
/ PRIOR APPLICATION NUMBER: US 60/067,740
/ PRIOR FILING DATE: 1997-12-02
/ PRIOR APPLICATION NUMBER: US 60/080,970
/ PRIOR FILING DATE: 1998-04-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-201-430-1
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
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RESULT 94
US-09-724-551-42
/ Sequence 42, Application US/09724551
/ Patent No. 6787637
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ APPLICANT: Bard, Frederique
/ APPLICANT: Vedock, Ted
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 15270J-4760US
/ CURRENT APPLICATION NUMBER: US/09/724,551
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US/09/580,018
/ PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-551-42

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 95
US-10-815-353-1
; Sequence 1, Application US/10815353
; Patent No. 6808712
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/815,353
; PRIOR FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-815-353-1

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 96
US-10-278-181-1
; Sequence 1, Application US/10278181
; Patent No. 6811988
; GENERAL INFORMATION:
; APPLICANT: Chojtier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOJTER-04302
; CURRENT APPLICATION NUMBER: US/10/278,181
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/731,460
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentln Ver. 2.0
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; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-278-181-1

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 97
US-10-816-529-1
; Sequence 1, Application US/10816529
; Patent No. 6818218
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,529
; PRIOR FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-816-529-1

Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30

RESULT 98
US-09-623-548A-955
; Sequence 955, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Birlon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
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Page 34

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; PRIOR FILING DATE: 1999-09-10
; FILE REFERENCE: 15270J-004720US
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 955
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-955
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYVHHQKLVFPAEDVGSNKGA 30
DB      1 DAEFRHDSGYVHHQKLVFPAEDVGSNKGA 30
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RESULT 99
US-09-623-548A-988
; Sequence 988, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Thibaudau, Karen
; APPLICANT: Holmes, Darren
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 988
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-988
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYVHHQKLVFPAEDVGSNKGA 30
DB      1 DAEFRHDSGYVHHQKLVFPAEDVGSNKGA 30
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RESULT 100
US-10-815-391-1
; Sequence 1, Application US/10815391
; Patent No. 6866849
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
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; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/815,391
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-815-391-1
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Query Match          100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYVHHQKLVFPAEDVGSNKGA 30
DB      1 DAEFRHDSGYVHHQKLVFPAEDVGSNKGA 30
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Search completed: April 20, 2006, 10:06:41
Job time : 49 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 20, 2006, 10:01:26 ; Search time 38 Seconds
(without alignments)
75.961 Million cell updates/sec

Title: US-10-666-423-1

Perfect score: 162
Sequence: 1 DAEFRHDSGYEVHHQKLVFFAEDYGSNKG 30

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	42	2	PN0512
2	162	100.0	57	2	AE0045
3	162	100.0	57	2	PE0045
4	162	100.0	57	2	DE0045
5	162	100.0	57	2	BE0045
6	162	100.0	57	2	GE0045
7	162	100.0	57	2	BE0045
8	162	100.0	82	2	PQ0438
9	162	100.0	695	1	AA9795
10	162	100.0	770	1	ORH044
11	143	88.3	695	2	A27485
12	143	88.3	695	2	S00550
13	143	88.3	747	2	UH0773
14	133	82.1	33	2	S23094
15	35.2	32.7	327	2	S11435
16	55	34.0	3063	2	JS0166
17	54	33.3	284	2	S04723
18	53.5	33.0	971	2	D70128
19	53	32.7	256	2	G96774
20	53	32.7	1555	2	UT0959
21	52	32.1	272	2	F70979
22	50.5	31.2	519	2	PC1072
23	49	30.2	488	2	S27652
24	49	30.2	527	2	AA3938
25	49	30.2	704	2	AA4287
26	48.5	29.9	330	2	AA6205
27	48.5	29.9	393	2	S59499
28	48.5	29.9	547	2	AD2250
29	48	29.6	703	2	B34434

30	48	29.6	1573	2	AF3514	glutamate synthase
31	47	29.0	175	2	F82486	conserved hypotet
32	47	29.0	180	2	T18161	hypothetical prote
33	47	29.0	291	2	P95015	glycosyl transfera
34	47	29.0	317	2	H97888	glycosyl transfera
35	47	29.0	489	2	AD2834	hypothetical prote
36	47	29.0	508	2	H97611	hypothetical prote
37	47	29.0	688	2	B86448	hypothetical prote
38	46.5	28.7	539	2	T39150	probable heat shoc
39	46.5	28.7	1068	2	T48756	mitochondrial nico
40	46	28.4	77	2	C97027	feoA-like protein,
41	46	28.4	219	2	S70311	hypothetical prote
42	46	28.4	311	2	AF1266	L-lactate dehydrog
43	46	28.4	311	2	AA1628	L-lactate dehydrog
44	46	28.4	372	2	G90983	GDP-D-mannose dehy
45	46	28.4	372	2	B85829	GDP-D-mannose dehy
46	46	28.4	708	2	T24727	hypothetical prote
47	46	28.4	1536	2	S59841	4-alpha-glucanotri
48	46	28.4	2178	2	S55805	alpha-toxin - Clo
49	45.5	28.1	297	2	G69525	formylmethanofuran
50	45.5	28.1	313	2	JT0960	polypyrrolin - pota
51	45.5	28.1	337	2	AB3603	3-methyl-2-oxobuta
52	45.5	28.1	427	2	JA0073	genome polypyrrolin
53	45.5	28.1	514	2	A36793	hypothetical prote
54	45.5	28.1	678	2	G71526	3-methyl-2-oxobuta
55	45	27.8	228	2	G87000	hypothetical prote
56	45	27.8	530	2	T23255	probable membrane
57	45	27.8	533	2	B84858	hypothetical prote
58	45	27.8	624	1	BHTLE	phosphoprotein pho
59	45	27.8	702	2	A34434	hemocyanin chain c
60	45	27.8	1104	2	A60999	arylphorin alpha c
61	45	27.8	1808	2	AB1847	serine/threonine k
62	44.5	27.5	252	2	AE1302	probable phosphopr
63	44.5	27.5	352	2	AE1674	probable phosphopr
64	44.5	27.5	317	2	T08962	hypothetical prote
65	44.5	27.5	392	2	T19869	hypothetical prote
66	44.5	27.5	436	2	A69662	UDP-N-acetylglucos
67	44.5	27.5	559	2	F71420	hypothetical prote
68	44.5	27.5	678	2	C81683	3-methyl-2-oxobuta
69	44.5	27.5	781	2	T36143	probable secreted
70	44	27.2	218	2	A55734	sodium channel, vo
71	44	27.2	274	2	A42737	sodium channel bet
72	44	27.2	274	2	A64978	hypothetical prote
73	44	27.2	284	2	S04278	hypoxanthine phosph
74	44	27.2	421	2	S29599	acrosin (EC 3.4.21
75	44	27.2	698	2	AB2427	hypothetical prote
76	44	27.2	702	2	C86268	FI3B4.2 protein -
77	44	27.2	1139	1	PAYBBS	alpha-a protein -
78	43.5	26.9	121	2	S48420	probable membrane
79	43.5	26.9	143	2	T13179	hypothetical prote
80	43.5	26.9	284	2	T21923	hypothetical prote
81	43.5	26.9	763	2	A13443	Na+/H+ antiporter
82	43.5	26.9	1141	2	T05068	glutamate synthase
83	43.5	26.9	1493	2	F70435	glutamate synthase
84	43	26.5	119	2	F69770	hypothetical prote
85	43	26.5	155	2	UC7732	tryptophan-plasma
86	43	26.5	308	2	S74834	hypothetical prote
87	43	26.5	339	2	AB1351	signal transductio
88	43	26.5	371	2	AD1201	N-acyl-L-amino aci
89	43	26.5	371	2	AB1559	N-acyl-L-amino aci
90	43	26.5	382	2	B86268	FI3B4.1 protein -
91	43	26.5	452	2	AA8452	hypothetical prote
92	43	26.5	489	2	A49368	catelase (EC 1.11.
93	43	26.5	494	2	C70940	probable codo prot
94	43	26.5	516	2	T10000	cytochrome P450 -
95	43	26.5	524	2	T09999	probable cytochrom
96	43	26.5	524	2	T09944	protein FI0A5.13 l
97	43	26.5	525	1	E96786	phosphoprotein pho
98	43	26.5	526	1	T45058	hypothetical prote
99	43	26.5	613	2	AB2834	hypothetical prote
100	43	26.5	629	2	S60385	probable membrane

ALIGNMENTS

RESULT 1

beta-amyloid protein - guinea pig (fragment)
P05012

C/Species: *Cavia porcellus* (guinea pig)

C/Date: 01-Dec-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: F60045

R/Johantone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment

A/Reference number: P05012; PMID:9329063; PMID:7685978

A/Accession: F60045

A/Molecule type: protein

A/Residues: 1-42 <SH>

A/Cross-references: UNIPARC:UPI00000315E8

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C/Keywords: alternative splicing; amyloid

Query Match

Best Local Similarity 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2, 8e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

DB 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

RESULT 2

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C/Species: *Canis lupus familiaris* (dog)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: A60045

R/Johantone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; PMID:92017079; PMID:1656157

A/Accession: A60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56125

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 162; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3, 9e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

DB 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 35

RESULT 3

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C/Species: *Sus scrofa domestica* (domestic pig)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C/Accession: F60045

R/Johantone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; PMID:92017079; PMID:1656157

A/Accession: F60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIDD:CAA3592.1; PID:

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 162; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 3, 9e-17;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

DB 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 35

RESULT 4

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C/Species: *Bos taurus* (cattle)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: D60045

R/Johantone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; PMID:92017079; PMID:1656157

A/Accession: D60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56124

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 162; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3, 9e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

DB 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 35

RESULT 5

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C/Species: *Ovis sp.* (sheep)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: E60045

R/Johantone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; PMID:92017079; PMID:1656157

A/Accession: E60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56130

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 162; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3, 9e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30

DB 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 35

RESULT 6

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C/Species: *Cavia porcellus* (guinea pig)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: G60045

R/Johantone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; PMID:92017079; PMID:1656157

A/Accession: G60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 162; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.9e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKGA 30
DB 6 DAEFRHDSGYEVHOKLVFPADVGSNKGA 35

RESULT 7

B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C/Species: Ursus maritimus (polar bear)
C/Date: 01-Dec-1992 #sequence, revision 01-Dec-1992 #text_change 09-Jul-2004
C/Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:g2165; PIDN:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 162; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.9e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKGA 30
DB 6 DAEFRHDSGYEVHOKLVFPADVGSNKGA 35

RESULT 8

P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1993 #sequence, revision 19-Oct-1995 #text_change 19-Oct-1995

C/Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Naroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: P00438; MUID:93075180; PMID:1445331

A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DNA>

A/Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 162; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 5.8e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKGA 30
DB 17 DAEFRHDSGYEVHOKLVFPADVGSNKGA 46

RESULT 9

A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A49795
R:Podilany, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

A>Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117; PMID:1905108

A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>

A/Cross-references: UNIPARC:UPI00002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PI
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 162; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 6.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKGA 30
DB 597 DAEFRHDSGYEVHOKLVFPADVGSNKGA 626

RESULT 10

Q8RHU4

Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inh

N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascul
protein precursor splice form APP(770)

C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence, revision 28-Jul-1995 #text_change 15-Sep-2000

C/Accession: S02260; S05194; A32277; A32260; A35486; I39452; I39451; I39453; I59562; A
4668; A28583; A29302; A60805; J10038; S06121; A60315; A59011; A38384; S29076; S38252;

R:Leinarte, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; B
Nucleic Acids Res. 17, 517-522, 1989

A>Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded
A:Reference number: S02260; MUID:89128427; PMID:2783775

A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288 'V', 365-770 <LEML>

A/Cross-references: UNIPARC:UPI00002A2F2; EMBL:X13466
A>Note: alternative splice form APP(695)

R:Leinarte, H.G.
submitted to the EMBL Data Library, November 1988

A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEML2>

A/Cross-references: UNIPARC:UPI000016A551; EMBL:X13466; NID:g35598; PIDN:CAA31830.1; P
A>Note: alternative splice form APP(695)

R:LaFaut, G.; Lahiri, D.K.; Salton, S.R.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A>Title: Characterization of the 5'-end region and the first two exons of the beta-pro
A:Reference number: A32277; MUID:89165870; PMID:2538123

A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>

A/Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:g341202; PIDN:AA
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.B.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simil
A:Reference number: A33260; MUID:89392030; PMID:2675837

A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>

A/Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:g178863; PIDN:AAA51768.1; PI
R:Jirelli, F.; Levy, E.; van Duinen, S.G.; Bocs, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Cross-references: UNIPARC:UPI0000149176
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R.Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: 139451; MUID:90263618; PMID:2110105
A:Accession: 139452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G176613; PIDN:AA59502.1; PID:
A:Accession: 139451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530 'OWMPVTPAFKAVGR' <YOS2>
A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G176608; PIDN:AA59501.1; PID:
R.Yoshikai S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Accession: 139453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEAV>
A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G176618; PIDN:AA51727.1; PID:
A:Note: a mutation with 693-Gln is presented
R.Murrell, J.; Farlow, M.; Gheut, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: 159562; MUID:92022553; PMID:1925564
A:Accession: 159562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: UNIPARC:UPI000011F7BA; GB:S57665; NID:G236720; PIDN:AA3991.1; PID:
R.Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
Arakhi, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: UNIPARC:UPI000011F7BB; GB:S45135; NID:G257377; PIDN:AA53645.1; PID:
A:Experimental source: familial Alzheimer disease family SB
A:Note: this sequence extracted from NCBI backbone (NCBI:P.115376)
R.Kam, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:G28525; PIDN:CAA60374.1; PID:
A:Note: alternative splice form APP(695)
R.Rodakis, N.K.; Kamakishima, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:G176539; PIDN:AA51722.1; PID:
A:Note: the authors translated the codon GAG for residue 647 as Asp
R.Goldberger, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <COL>
A:Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:G178706; PIDN:AA35540.1; PID:
A:Experimental source: brain
R.Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van K
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near t
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TRAN1>
A:Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:G177957; PIDN:AA51564.1; PID:
R.Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muehl
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A:Reference number: 802638; MUID:88296437; PMID:2900137
A:Accession: 802638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
A:Cross-references: UNIPARC:UPI0000035AB0
R.Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nev
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
A:Reference number: 800707; MUID:88122640; PMID:2893290
A:Accession: 800707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TRAN2>
A:Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PI
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R.Ponte, P.; Gonzalez-Dewhilt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; E
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <RO2>
A:Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAN
A:Note: alternative splice form APP(751)
R.Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-533, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibiti
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: UNIPARC:UPI00001455B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R.Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashb
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIR1>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Cross-references: UNIPARC:UPI0000174094
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 A:Cross-references: UNIPARC:UPI0000174094
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954; PMID:2893379
 A:Accession: A31087
 A:Molecule type: mRNA

Query Match 100.0%; Score 162; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.9e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30
 |||||
 Db 672 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 701

RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 A:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
 A:Reference number: A27485; MUID:88106489; PMID:3322280
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Bergh, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; MUID:92096458; PMID:1756177
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: UNIPARC:UPI000002A2F9; EMBL:A59379
 R:izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A:Reference number: I49485; MUID:92209998; PMID:1555768
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BA01456.1; PID:
 C:Genetics: 16C3
 A:Map position: 16C3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 88.3%; Score 143; DB 2; Length 695;
 Best Local Similarity 90.0%; Pred. No. 4.1e-13;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30
 |||||
 Db 597 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 626

RESULT 12
 S00550
 Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 A:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat bra
 A:Reference number: S00550; MUID:88312583; PMID:2900758
 A:Accession: S00550
 A:Molecule type: mRNA

A:Residues: 1-695 <SHI>
 A:Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PI
 R:Schubert, D.; Schroeder, R.; LaCordiere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan cor
 A:Reference number: A41245; MUID:88264430; PMID:2966652
 A:Accession: A41245
 A:Molecule type: protein
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A:Cross-references: UNIPARC:UPI0000177FD
 A:Note: evidence for heparan sulfate attachment
 R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.
 A:Reference number: S46251; MUID:94320627; PMID:7913895
 A:Contents: annotation; copper binding sites
 A:Note: rat peptides were isolated but not sequenced
 R:Potempa, A.; Styles, U.; Mehta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat br
 A:Reference number: A39820; MUID:91217087; PMID:1673681
 A:Accession: A39820
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-32 <POR>
 A:Cross-references: UNIPARC:UPI0000177FE
 A:Experimental source: brain
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 P:625-648/Domain: transmembrane #status predicted <TM>

Query Match 88.3%; Score 143; DB 2; Length 695;
 Best Local Similarity 90.0%; Pred. No. 4.1e-13;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 30
 |||||
 Db 597 DAEFRHDSGYEVHOKLVFPAEDVGSNKGA 626

RESULT 13
 JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 A:Accession: JH0773
 R:Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmenta
 A:Reference number: JH0773; MUID:93129227; PMID:1282805
 A:Accession: JH0773
 A:Molecule type: mRNA
 A:Residues: 1-747 <OKA>
 A:Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:g263150; PIDN:AAB24853.1; PI
 A:Experimental source: larva
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid
 P:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 88.3%; Score 143; DB 2; Length 747;
 Best Local Similarity 83.3%; Pred. No. 4.5e-13;
 Matches 25; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGA 30
Db 649 DSEYRHDTAYEVHHQKLVFAEAVGSNKGA 678

RESULT 14
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198; PMID:1618299
A:Accession: S23094
A:Molecule type: Protein
A:Residues: 1-33 <KOJ>
A:Cross-references: UNIPARC:UPI00001777FB
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 3

Query Match 82.1%; Score 133; DB 2; Length 33;
Best Local Similarity 89.3%; Pred. No. 4,3e-13;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNK 28
Db 6 DAEFRHDSGYEVHHQKLVFAEDVGSNK 33

RESULT 15
S11435
genome polypeptide - potato virus Y (fragment)
N:Contains: coat protein, N1D protein
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C:Accession: S11435; S11549; JCI526
R:Zhou, X.R.; Fang, R.X.; Wang, C.Q.; Mang, K.Q.
Nucleic Acids Res. 18, 5854, 1990
A:Title: cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).
A:Reference number: S11435; MUID:91016851; PMID:2216735
A:Accession: S11435
A:Molecule type: mRNA
A:Residues: 1-327 <ZHOU>
A:Cross-references: UNIPROT:P21294; UNIPARC:UPI000017871F; EMBL:X54058
R:Zhou, X.R.
submitted to the EMBL Data Library, July 1990
A:Reference number: S11549
A:Accession: S11549
A:Molecule type: mRNA
A:Residues: 1-90, 'E', '92-327 <ZHOU>
A:Cross-references: UNIPARC:UPI000013166; EMBL:X54058; NID:961219; PIDN:CAA37993.1; PID
R:Ohshima, K.; Hataya, T.; Sano, T.; Inoue, A.K.; Shikata, E.
Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991
A:Title: Comparison of biological properties, serological characteristics and amino acid
A:Reference number: JCI526
A:Accession: JCI526
A:Molecule type: genomic RNA
A:Residues: 61-68, 'E', '71-73, 'ES', '76-111, 'S', '113-201, 'E', '203-327 <OHS>
A:Cross-references: UNIPARC:UPI0000178720
C:Genetics:
A:Start codon: GCA
C:Superfamily: tobacco etch virus genome polypeptide
C:Keywords: coat protein; polypeptide; status predicted <CO>

Query Match 35.2%; Score 57; DB 2; Length 327;
Best Local Similarity 53.1%; Pred. No. 1.1;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNK 28

Db 47 DAEFRHDSGYEVHHQKLVFAEDVGSNK 72

RESULT 16
S04723
genome polypeptide - potato virus Y (strain N)
N:Contains: 31K protein; 38K protein; capsid protein; cytoplasmic inclusion protein; ge
olymerase (BC 2.7.7.48) core, nuclear inclusion protein a
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Feb-2001
C:Accession: S04723; PS0317
R:Robaglia, C.; Durand-Rardif, M.; Tronchet, M.; Boudazin, G.; Astier-Manifacier, S.; C
J. Gen. Virol. 70, 935-947, 1989
A:Title: Nucleotide sequence of potato virus Y (N strain) genomic RNA.
A:Reference number: S04723; MUID:89279275; PMID:2732709
A:Accession: S04723
A:Molecule type: Protein
A:Residues: 1-3063 <ROB>
A:Cross-references: UNIPARC:UPI0000178735
A:Accession: PS0317
A:Molecule type: Protein
A:Residues: 1158-1163;2797-2812, 'Q', '2814-2816 <RO2>
A:Cross-references: UNIPARC:UPI0000178735
C:Superfamily: tobacco etch virus genome polypeptide
C:Keywords: ATP; cysteine proteinase; genome-linked protein; glycoprotein; hydrolase; n
F:1-75/Products: 31K protein #status predicted <31K>
F:175-824/Products: helper component #status predicted <HPC>
F:309-340/Products: zinc binding #status predicted
F:825-1157/Products: 38K protein #status predicted <38K>
F:1158-1791/Products: cytoplasmic inclusion protein #status predicted <CIP>
F:1137-1332/Products: nucleotide-binding motif A (P-loop)
F:1131-1334/Products: DEXA motif B
F:1792-1843/Products: genome-linked protein #status predicted <GRP>
F:1844-2275/Products: nuclear inclusion protein b #status predicted <NIB>
F:2276-2796/Products: nuclear inclusion protein b #status predicted <NIB>
F:2797-3063/Products: capsid protein #status predicted <CAP>
F:450-744/Products: carboxylate (Asn) (covalent) #status predicted
F:1212/Products: phosphate-RNA (Tyr) (covalent) #status predicted
F:1212, 2198/Products: Cys, His #status predicted

Query Match 34.0%; Score 55; DB 2; Length 3063;
Best Local Similarity 53.1%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNK 28
Db 2783 DAEFRHDSGYEVHHQKLVFAEDVGSNK 2808

RESULT 17
S04723
genome polypeptide - potato virus Y (strain O) (fragment)
N:Contains: coat protein, replicase
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04723
R:Bravo-Almonacid, F.; Mentaberry, A.N.
Nucleic Acids Res. 17, 4401, 1989
A:Title: Nucleotide cDNA sequence coding for the PVYO coat protein.
A:Reference number: S04723; MUID:89296509; PMID:2740238
A:Accession: S04723
A:Molecule type: genomic RNA
A:Status: translation not shown
A:Cross-references: UNIPROT:P1897; UNIPARC:UPI000013166A; EMBL:X14136; NID:961445; PIR
C:Superfamily: tobacco etch virus genome polypeptide
C:Keywords: polypeptide

Query Match 33.3%; Score 54; DB 2; Length 284;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

A:Accession: PC1072
A:Molecule type: mRNA
A:Residues: 1-519 <LUY>
A:Cross-references: UNIPROT:O8JUZ2, UNIPROT:O72606, UNIPROT:Q85105, UNIPROT:Q85274, UNIPROT:Q85275
A:Experimental source: N strain
A:Genetics:
A:Gene: NIB

Query Match 31.2% Score 50.5; DB 2; Length 519;
Best Local Similarity 73.3%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 DAERFHDGSEVHHQ 15
DB 506 DDEFFEDS-YEVHHQ 519

RESULT 23
S27652
probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) - Pseudomonas sp.
C:Species: Pseudomonas sp.
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: C42971; S27652
R:Pearson, J.A.; Lu, J.Y.; Geiselsoder, J.; Graham-Lorence, S.; Carmona, C.; Witney, R.
J. Biol. Chem. 267, 14193-14203, 1992
A:Title: Cytochrome P-450exp. Isolation and purification of the protein and cloning and
A:Reference number: A42971; MUID:92332528; PMID:1629218
A:Accession: C42971
A:Structure: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-488 <PER>
A:Cross-references: UNIPROT:P3J008, UNIPARC:UPI000012928E; EMBL:M91440; NID:g151584; PMID:108473
A:Note: sequence extracted from NCBI backbone (NCBI:P108473)
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C:Keywords: NAD; oxidoreductase

Query Match 30.2% Score 49; DB 2; Length 488;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 12; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

OY 6 HDGSEVHHQKVPFADY---GSNKG 29
DB 305 HESVYEARDKLVAVAGNVVIGDSQPG 352

RESULT 24
A43938
Pseudomonas cytochrome oxidase (EC 1.9.3.2) - Pseudomonas stutzeri (strain JM300)
N:Alternate names: cytochrome cdl; heme-type nitrite reductase
C:Species: Pseudomonas stutzeri
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A43938; A39735
R:Smith, G.B.; Tiedje, J.M.
Appl. Environ. Microbiol. 58, 376-384, 1992
A:Title: Isolation and characterization of a nitrite reductase gene and its use as a probe
A:Reference number: A43938; MUID:92171504; PMID:1539983
A:Accession: A43938
A:Molecule type: DNA
A:Residues: 1-527 <SMT>
A:Cross-references: UNIPROT:O52519; UNIPARC:UPI00001751BC
A:Note: sequence extracted from NCBI backbone (NCBI:P48073)
R:Weeg-Messene, R.; Wu, W.; Ye, R.W.; Tiedje, J.M.; Chang, C.K.
J. Biol. Chem. 266, 7496-7502, 1991
A:Title: Purification of cytochrome cd-1 nitrite reductase from Pseudomonas stutzeri JM300
A:Reference number: A39735; MUID:91210258; PMID:1850410
A:Accession: A39735
A:Molecule type: protein
A:Residues: 1-56 <MEB>
A:Cross-references: UNIPARC:UPI00001751BD
C:Genetics:
A:Gene: nirs

C:Superfamily: Pseudomonas cytochrome oxidase; cytochrome c6 homology
C:Keywords: chromoprotein; electron transfer; heme; heterodimer; iron; metalloprotein; d

F.11-93/Domain: cytochrome c6 homology <C6>
F.21-24/Binding site: heme (Cys) (covalent) #status predicted
F.25/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 30.2% Score 49; DB 2; Length 527;
Best Local Similarity 37.9% Pred. No. 28;
Matches 11; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

CY 2 AEFRRDSCYEYVHQKLVFPAEDVGSNKCA 30
DB 301 AKFTHDGMDSHRTFWYAN--ASNKAA 327

RESULT 25

AJ4287
storage protein 2 - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
C:Accession: AJ4287
R.Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.
J. Biol. Chem. 264, 11020-11025, 1989
A:Title: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx m
A:Reference number: AJ4287; MUID:89291839; PMID:2544581
A:Accession: AJ4287
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-704 <FU>
A:Cross-references: UNIPROT:P20613; UNIPARC:UPI000017887B
C:Superfamily: arylphorin

Query Match 30.2% Score 49; DB 2; Length 704;
Best Local Similarity 44.4% Pred. No. 39;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 10 YEYHHOKLVPAEDVGSN 27
DB 218 YNNEBQRLLTYTEDIGAN 235

RESULT 26

A26205
coat protein precursor - pepper mottle virus
C:Species: pepper mottle virus
C:Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26205
R.Dougherty, W.G.; Allison, R.F.; Parks, T.D.; Johnston, R.E.; Field, M.J.; Armstrong,
Virology 146, 282-291, 1985
A:Title: Nucleotide sequence at the 3' terminus of pepper mottle virus genomic RNA: evl
A:Reference number: A26205
A:Accession: A26205
A:Molecule type: genomic RNA
A:Residues: 1-330 <DOU>
A:Cross-references: UNIPROT:P07993; UNIPARC:UPI0000127D81
C:Superfamily: tobacco etch virus genome polyprotein

Query Match 29.9% Score 48.5; DB 2; Length 330;
Best Local Similarity 73.3% Pred. No. 20;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

CY 1 DAEFRHDSGYEVHHQ 15
DB 50 DDEFECDS-YEVHHQ 63

RESULT 27

S59499
cellulase egII - smut fungus (Ustilago maydis)
C:Species: Ustilago maydis (corn smut)
C:Date: 20-Jul-1986 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S59499
R.Schauwecker, F.; Wanner, G.; Kahmann, R.
Biol. Chem. Hoppe-Seyler 376, 617-625, 1995
A:Title: Filament-specific expression of a cellulase gene in the dimorphic fungus Ustil

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-180 <GB>
A/Cross-references: UNIPROT:Q41141; UNIPARC:UPI00000F287D; EMBL:U42580; NID:94028896; PI
A/Experimental source: specific host *Chlorella* strain NC64A
C/Genetics:
A/Note: A639L

Query Match 29.0%; Score 47; DB 2; Length 180;
Best Local Similarity 39.3%; Pred. No. 17;
Matches 11; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 1 DA6FRHDSGYEVHOKLVFPAEDVGSNK 28
DB 146 DSELDHVDENEVEEENSFVAEDVAEEK 173

RESULT 33
P95015
glycoyl transferase, family 2 SP0136 [imported] - Streptococcus pneumoniae (strain TIGR
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: P95015
R/Teteljin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A./Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: P95015
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-291 <KUR>
A/Cross-references: UNIPROT:Q97T23; UNIPARC:UPI00000512F6; GB:AE005672; PIDN:AAK74319.1;
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP0136
C/Superfamily: Neisseria meningitidis glycoyl transferase A

Query Match 29.0%; Score 47; DB 2; Length 291;
Best Local Similarity 42.9%; Pred. No. 29;
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 6 HDSCGYEVHOKLVFPAEDVGS 26
DB 58 H0F0YTHRIKLIISNEDLGA 78

RESULT 34
H97888
glycoyl transferase, family 2 [imported] - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: H97888
R/Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balaz, R.H.; Jaskunas, S.R.;
A./Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: H97888
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-317 <KUR>
A/Cross-references: UNIPROT:Q8DRG7; UNIPARC:UPI00000E33BF; GB:AE007317; PIDN:AAK98940.1;
C/Genetics:
A/Gene: glycoyltransferase
C/Superfamily: Neisseria meningitidis glycoyl transferase A

Query Match 29.0%; Score 47; DB 2; Length 317;
Best Local Similarity 42.9%; Pred. No. 32;

Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 6 HDSCGYEVHOKLVFPAEDVGS 26
DB 58 H0F0YTHRIKLIISNEDLGA 78

RESULT 35
AD2834
hypothetical protein mure [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
C/Accession: AD2834
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A./Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AD2834
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-489 <KUR>
A/Cross-references: UNIPROT:Q6UDM3; UNIPARC:UPI000012F98C; GB:AB008688; PIDN:AL43090.1,
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: mure
A/Map position: circular chromosome
C/Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 29.0%; Score 47; DB 2; Length 489;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 FRHDSGYEVHOKLVF 19
DB 274 FRHKOMIEVHDSGVIF 289

RESULT 36
H97611
hypothetical protein AGR_C_3809 [imported] - Agrobacterium tumefaciens (strain C58, Cer
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
C/Accession: H97611
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A./Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: H97611
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-508 <KUR>
A/Cross-references: UNIPARC:UPI00001643BA; GB:AE007869; PIDN:AAK87849.1; PID:GI5157233;
C/Genetics:
A/Gene: AGR_C_3809
A/Map position: circular chromosome
C/Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 29.0%; Score 47; DB 2; Length 508;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 FRHDSGYEVHOKLVF 19
DB 293 FRHKOMIEVHDSGVIF 308

RESULT 37
B86448

hypothetical protein FSD14.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B66448
R:Thelogiis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Weng, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B66448
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-688 <STO>
A:Cross-references: UNIPROT:Q9LQW5; UNIPARC:UPI00000ABF54; GB:AE005172; NID:98920608; PI C:Genetics:
A:Map position: 1

Query Match 29.0%; Score 47; DB 2; Length 688;
Best Local Similarity 40.0%; Pred. No. 76;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVG 25
DB 363 DDEKRDHDSFLQSLHHCICFBSAG 387

RESULT 38
T39150
Probable heat shock transcription factor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C:Accession: T39150
R:Oliver, K.; Harris, D.; Bartell, B.G.; Rajandram, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: 221748
A:Accession: T39150
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-539
A:Cross-references: UNIPROT:O14283; UNIPARC:UPI000013235A; EMBL:Z99168; PIDN:CBM16301.1;
A:Experimental source: strain 972h-; cosmid c8C9
C:Genetics:
A:Gene: SPDB:SPAC8C9.14
A:Map position: 1
A:Introns: 10/3; 40/3; 67/2; 86/3
C:Superfamily: heat shock transcription factor with receiver domain

Query Match 28.7%; Score 46.5; DB 2; Length 539;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 3 EFRHDSGYEVHHQKLV 18
DB 89 EFRHDD-FOLHKKDL 103

RESULT 39
T48756
mitochondrial nicotinamide nucleotide transhydrogenase-related protein [imported] - Neurospora crassa
N:Alternate names: protein 13E11.40
C:Species: Neurospora crassa
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: T48756
R:Schulte, U.; Aign, V.; Hohnel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
A:Reference number: 224541
A:Accession: T48756

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1068 <SCH>
A:Cross-references: UNIPROT:Q9P712; UNIPARC:UPI0000175045; EMBL:AL353820; GSPDB:GND00112
A:Experimental source: cosmid contig 13E11; strain 74
C:Genetics:
A:Gene: NCSP:13E11.40
A:Map position: 2
A:Introns: 37/1; 368/1; 1031/1
C:Superfamily: NAD(P)+ transhydrogenase (B-specific); alanine dehydrogenase homology; 1 logy
C:Keywords: mitochondrion
F:56-353/Domain: alanine dehydrogenase homology <ALA>

Query Match 28.7%; Score 46.5; DB 2; Length 1068;
Best Local Similarity 48.1%; Pred. No. 1.5e+02;
Matches 13; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSN 27
DB 98 EAEF-HDSAVTATGATIVESASDVWNN 123

RESULT 40
C97027
FeoA-like protein, involved in iron transport CAC1030 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97027
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lec J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1 A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: C97027
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <KDR>
A:Cross-references: UNIPROT:Q97K89; UNIPARC:UPI00000CA073; GB:AE001437; PIDN:AAK79006.1
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1030

Query Match 28.4%; Score 46; DB 2; Length 77;
Best Local Similarity 43.3%; Pred. No. 9.5;
Matches 13; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKA 30
DB 16 DAEVDRDITGTEVMCKLM----EMGRNNGA 41

RESULT 41
S70311
hypothetical protein YAR002c-a - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
C:Accession: S70311
R:Bussey, H.
submitted to the EMBL Data Library, May 1996
A:Reference number: S70311
A:Accession: S70311
A:Molecule type: DNA
A:Residues: 1-219 <BUS>
A:Cross-references: UNIPARC:UPI0000052F10; EMBL:L22015; NID:G1339990; PIDN:AAC04958.1;
C:Genetics:
A:Gene: SGD:ERPL; MIPS:YAR002c-a
A:Cross-references: SGD:S0002129
A:Map position: 1R
C:Superfamily: conserved hypothetical protein YHR110W

Query Match 28.4%; Score 46; DB 2; Length 219;
Best Local Similarity 38.2%; Pred. No. 30;

Matches 13: Conservative 2: Mismatches 13: Indels 6: Gaps 1:

QY 1 DAERHDSGYEVHOK-----LVFAPEDVGSNK 28

Db 74 DIETFPDNDLVVHOKSGASGDLTFLASDGEHK 107

RESULT 42

AF1266
L-lactate dehydrogenase homolog lml1534 [imported] - *Listeria monocytogenes* (strain EGD-C)
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AF1266
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kuntz, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tlieriez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A./Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AF1266
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <GLA>
A/Cross-references: UNIPROT:O8Y6Z6; UNIPARC:UPI0000551D9; GB:NC_003210; PIDN:CAC9612.1
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: lml1534
C/Superfamily: L-lactate dehydrogenase

Query Match 28.4%; Score 46; DB 2; Length 311;

Best local similarity 50.0%; Pred. No. 44;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHOK 16

Db 214 ETARDTGERIYNOK 227

RESULT 43

AH1628
L-lactate dehydrogenase homolog lml1569 [imported] - *Listeria innocua* (strain C11p11262)
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AH1628
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kuntz, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tlieriez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A./Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AH1628
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <GLA>
A/Cross-references: UNIPROT:Q92B10; UNIPARC:UPI00000C5CC; GB:AL592022; PIDN:CAC96800.1
A/Experimental source: strain C11p11262
C/Genetics:
A/Gene: lml1569
C/Superfamily: L-lactate dehydrogenase

Query Match 28.4%; Score 46; DB 2; Length 311;

Best local similarity 50.0%; Pred. No. 44;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHOK 16

Db 214 ETARDTGERIYNOK 227

RESULT 44

G90983
GDP-D-mannose dehydratase [imported] - *Escherichia coli* (strain 0157:H7, substrain R1MD)
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004
C/Accession: G90983
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7 and gen
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: G90983
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-372 <HAY>
A/Cross-references: UNIPROT:O85339; UNIPARC:UPI00000D5DB; GB:BA000007; PIDN:BA936262.1
A/Experimental source: strain 0157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: ECE2839
C/Superfamily: GDP-D-mannose 4,6 dehydratase

Query Match 28.4%; Score 46; DB 2; Length 372;

Best local similarity 75.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEFRLDNGYEVH 13

Db 19 AEFRLDNGYEVH 30

RESULT 45

B85829
GDP-mannose dehydratase [imported] - *Escherichia coli* (strain 0157:H7, substrain EDL933)
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 12-Jul-2004
C/Accession: B85829
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, J.; Flier, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; DiMantanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7.
A/Reference number: AB5480; MUID:21074935; PMID:11206551
A/Accession: B85829
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-372 <STO>
A/Cross-references: UNIPROT:O85339; UNIPARC:UPI00000D5DB; GB:AE005174; MUID:g12516222;
A/Experimental source: strain 0157:H7, substrain EDL933
C/Genetics:
A/Gene: Z3198
C/Superfamily: GDP-D-mannose 4,6 dehydratase

Query Match 28.4%; Score 46; DB 2; Length 372;

Best local similarity 75.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEFRLDNGYEVH 13

Db 19 AEFRLDNGYEVH 30

RESULT 46

T24727
hypotheoretical protein T09A5.12 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T24727
R/Lightning, J.
submitted to the EMBL Data Library, August 1994
A/Reference number: Z19928
A/Accession: T24727
A/Status: preliminary; translated from GB/EMBL/DDbJ
A/Molecule type: DNA
A/Residues: 1-708 <WIL>

Query Match 28.4%; Score 46; DB 2; Length 372;

Best local similarity 75.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


```
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: J0960
R:Hidaka M.
Submitted to JIPID, November 1991
A:Reference number: J0959
A:Accession: J0960
A:Molecule type: genomic RNA
A:Releasers: 1-313 <HID>
A:Cross-references: UNIPROT:Q85259, UNIPARC:UPI000018787B
A:Experimental source: necrotic strain T
A:Superfamily: tobacco etch virus genome polypeptide
A:Keywords: polypeptide
E:46-313/Product: coat protein #status predicted <CNA>
```

Query Match	28.1%	Score	45.5	DB	2	Length	313
Best Local Similarity	66.7%	Pred.	No. 53				
Matches	10	Conservative	1	Mismatches	3	Indels	1
						Gaps	1

QY	1	DAEFRHDSGYEVHHQ	15
Db	33	DDEFECDT-YEVHHQ	46

```

RESULT 51
AB3603
3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) [imported] - Brucella mel
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 12-Jul-2004
C:Accession: AB3603
R:Devechko, V.G.; Kapatal, V.; Redkar, R.V.; Patra, G.; Mjjer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.;
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:1175688
A:Accession: AB3603
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <KUN>
A:Cross-references: UNIPROT:Q8YB9; UNIPARC:UPI00000585D8; GB:AE008918; PTDN:AAU53989.1/
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10747
A:Map position: II
C:Superfamily: pyruvate dehydrogenase, E1 component, beta subunit
C:Keywords: oxidoreductase

```

Query Match	28.1%	Score 45.5	DB 2	Length 337
Best Local Similarity	55.0%	Pred. No. 36		
Matches 11	Conservative 1	Mismatches 7	Indels 1	Gaps 1
Oy	6 HDSGYEVHHQKLVFFAEDVG	25		
Db	14 HDIAME-RDQKRVVFEEDVG	32		

RESULT 52

JA0073 genome polyprotein - potato virus Y (strain N) (fragment)

C|Species: potato virus Y, PVY

A|Note: host Nicotiana benthamiana

C|Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Dec-2004

C|Accession: JA0073; PS0281

R|van der Vlugt, R.; Allefs, S.; de Haan, P.; Goldbach, R.

J. Gen. Virol. 70, 229-233, 1989

A|Title: Nucleotide sequence of the 3'-terminal region of potato virus YN RNA.

A|Reference number: JA0073; MUID:89279156; PMID:2732687

A|Accession: JA0073

A|Molecule type: genomic RNA

A|Residues: 1-427 <VMA>

A|Cross-references: UNIPROT:Q85265; UNIPROT:Q85104; UNIPARC:UP10000178719

A|Accession: PS0281

A|Molecule type: protein

A|Residues: 161-182 <VA2>

A;Cross-references: UNIPARC:UPI000017871A
C;Keywords: polypeptide
F;161-427/Product: coat protein #status experimental <CPP>

Query Match	28.1%	Score 45.5	DB 2	Length 427
Best Local Similarity	66.7%	Pred. No. 75		
Matches 10	Conservative 1	Mismatches 3	Indels 1	Gaps 1

```
QY      1 DAEFRHDSGYEVHHQ 15
        | | | : | | | | |
Db      147 DDEFECDT-YEVHHQ 160
```

RESULT 53
A36793
hypothetical protein 64 - ictalurid herpesvirus 1 (strain auburn 1)
CISpecies: ictalurid herpesvirus 1
A>Note: host ictalurid punctatus (Channel catfish)
CDate: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
CAccession: A36793
R:Davidson, A.J.
submitted to GenBank, January 1992
A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804
A:Accession: A36793
A:Molecule type: DNA
A:Residues: 1-514 <DNA>
A:Cross-references: UNIPROT:Q00156; UNIPARC:UPI00001355E9; GB:M75136; NID:G9331209; PIDD
R:Davidson, A.J.
Virology 186, 9-14, 1992
A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; MUID:92087490; PMID:1177613
A:Contents: annotation
A>Note: neither protein nor nucleic acid sequence is given
C:Genetics:
A:Gene: 64
CISuperfamily: ictalurid herpesvirus 1 hypothetical protein 64

	Query Match	Similarity	28.1%	Score 45.5	DB 2	Length 514
	Best Local	Similarity	31.0%	Pred. No. 92		
	Matches	9	Conservative 10	Matches 7	Indels 3	Gaps 2
Qy	4	FRHDSGYEVHHQKLVFF--AEVDG-SNKG	29			
	:	:	:	:	:	:
	:	:	:	:	:	:
Db	365	YRNHKKYMHARVIFEFHMSISIFTEHG	393			

RESULT 54
 G71526
 3-methyl-2-oxobutanate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain pdhaA
 M.ALternate names: oxoisovalerate dehydrogenase
 C.Species: Chlamydia trachomatis
 C.Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
 C.Accession: G71526
 R.Stephans, R.S.; Kalman, S.; Lammell, C.J.; Fan, Y.; Marathe, R.; Aravind, L.; Mitchell
 Science 282, 754-759, 1998
 A.Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
 A.Reference number: A71570; MUID:9900809; PMID:9784136
 A.Accession: G71526
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-678 <ARR>
 A.Cross-references: UNIPROT:O84344; UNIPARC:UPI00000D7604; GB:AE001307; GB:AE001273; NIT
 A.Experimental source: serotype D, strain UW-3/Cx
 C.Genetics:
 A.Gene: pdhA/B
 C.Keywords: oxidoreductase

 Query Match 28.1%, Score 45.5; DB 2; Length 678;
 Best Local Similarity 40.7%; Pred. NO. 1.2e+02;
 Matches 11; Conservative 2; Mismatches 7; Indels 1;

QY 3 EFRHDSGYEVHHQKLVFFAEDVGSNKG 29

Db 364 EMGRDPG-----VVVFGEDVAGKNG 363

RESULT 55

G87000

probable membrane protein [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: G87000

R:Coile, S.T.; Sigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holtzman, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: G87000

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-228 <STD>

A:Cross-references: UNIPROT:Q49673; UNIPARC:UPI00000D4398; GB:AL450380; NID:g13092860; F:G:Genetics:

A:Gene: ML0734

Query Match 27.8%; Score 45; DB 2; Length 228;

Best Local Similarity 50.0%; Pred. No. 44;

Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 79 FRDRGGRERHNEALLFFA 96

RESULT 56

T23255

hypothetical protein K03A11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T23255

R:Swaburne, J.

submitted to the EMBL Data Library, July 1996

A:Reference number: Z19717

A:Accession: T23255

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-530 <MTL>

A:Cross-references: UNIPROT:Q21167; UNIPARC:UPI000007F7E0; EMBL:Z77133; PIDN:CAB00864.1

A:Experimental source: clone K03A11

C:Genetics:

A:Gene: CESP:K03A11.4

A:Map position: X

A:Introns: 151/2; 200/2; 233/2; 271/1; 319/1; 356/3; 374/3; 443/3; 475/3

Query Match 27.8%; Score 45; DB 2; Length 530;

Best Local Similarity 44.4%; Pred. No. 1.1e+02;

Matches 12; Conservative 6; Mismatches 7; Indels 2; Gaps 2;

Db 309 SEF-HDYGVRVNRKFGVWALDIGHN 334

RESULT 57

B84858

phosphoprotein phosphatase (EC 3.1.3.16) At2g42810 [similarity] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 28-Apr-2003

C:Accession: B84858

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Gnanapavan, S.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, D.

Nature 402, 761-768, 1999

```

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617157
A:Accession: B84858
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-533 <STO>
A:Cross-references: UNIPARC:UPI0000044D6A; GB:AB002093; NID:g4512673; PIDN:AA021727.1;
C:Genetics:
A:Gene: At2g42810
A:Map position: 2
C:Superfamily: protein phosphatase 5; phosphoesterase core homology; phosphoprotein pka
C:Keywords: phosphoric monoester hydrolase
Query Match 27.8% Score 45; DB 2; Length 533;
Best Local Similarity 53.3% Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 8; Indels 6; Gaps 3;
Cy 7 DSGEYVHHQ-GL--VFPAR---DVGSNKGK 30
Db 466 DGEYVEHDKLITVFSAPNYCDQMGNKGA 495
RESULT 58
BHTLE
hemocyanin chain e - American tarantula (Eurytelma californica)
C:Species: Eurytelma californica
C:Date: 15-Nov-1994 #sequence revision 31-Mar-1992 #text change 09-Jul-2004
C:Accession: S06701; A35772; S13441; A02566; A24179; B37975; S08107
R:Voll, W.M.M.
submitted to the EMBL Data Library, August 1989
A:Reference number: S06701
A:Accession: S06701
A:Molecule type: DNA
A:Residues: 1-624 <VOL>
A:Cross-references: UNIPROT:P02242; UNIPARC:UPI000016B89F; EMBL:X16650; NID:g9249; PIDN:
R:Voll, W. Voll, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 5312-5316, 1990
A:Title: Characterization of the gene encoding the hemocyanin subunit e from the tarant
A:Reference number: A35772; MUID:90319102; PMID:2371273
A:Accession: A35772
A:Molecule type: DNA
A:Residues: 1-64;604-624 <VOL2>
A:Cross-references: UNIPARC:UPI000017391F; UNIPARC:UPI0000173920
R:Voll, R.; Feldmaier-Fuchs, G.
J. Biol. Chem. 265, 19447-19452, 1990
A:Title: Arthropod hemocyanins. Molecular cloning and sequencing of cDNAs encoding the
A:Reference number: A37975; MUID:91060544; PMID:2246235
A:Accession: S13441
A:Molecule type: mRNA
A:Residues: 1-624 <VOI>
A:Cross-references: UNIPARC:UPI000016B89F; EMBL:X16894; NID:g9268; PIDN:CAA34772.1; PID
R:Schneider, H.J.; Drexel, R.; Feldmaier, G.; Linz, B.; Lotzspich, F.; Henseken, A.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1357-1381, 1983
A:Title: Hemocyanins in spiders, XVIII[1]. Complete amino-acid sequence of subunit e fr
A:Reference number: A02566; MUID:84059635; PMID:6357986
A:Accession: A02566
A:Molecule type: protein
A:Residues: 2-29, 'R', 31-46, 'D', 48-79, 'K', 81-90, 'H', 92-110, 112-159, 'K', 161-216, 'H', 218-2
A:Cross-references: UNIPARC:UPI0000173921
C:Genetics:
A:Insertions: 65/1; 137/3; 206/2; 338/3; 381/3; 426/3; 489/1; 560/3
C:Superfamily: hemocyanin
C:Keywords: copper; hemolymph; oxygen carrier
F:2-624/Product: hemocyanin chain e #status experimental <Mat>
F:2-150/Domain: 1 <DO1>
F:151-374/Domain: 2 <DO2>
F:375-624/Domain: 3 <DO3>
F:169,173,200/Binding site: copper (His) #status predicted
F:320,324,360/Binding site: copper (His) #status predicted
Query Match 27.8% Score 45; DB 1; Length 624;
Best Local Similarity 66.7% Pred. No. 1.3e+01;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 16 KLVEFADVGSN 27
||:|||||:
DB 155 KLAVEREDVGTN 166

RESULT 59
A34434
arylphorin alpha chain precursor - tobacco hornworm
C/Species: Manduca sexta (tobacco hornworm)
C/Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34434
R/Willett, E.; Wang, X.Y.; Wells, M.A.
J. Biol. Chem. 264, 19052-19059, 1989
A/Title: cDNA and gene sequence of Manduca sexta arylphorin, an aromatic amino acid-rich
A/Reference number: A34434; MUID:90037032; PMID:2808410
A/Accession: A34434
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-702 <WIL>
A/Cross-references: UNIPROT:P14296; UNIPARC:UPI00001260D5; GB:M28396; EMBL:J05092; NID:G
C/Superfamily: arylphorin

Query Match 27.8%; Score 45; DB 2; Length 702;
Best Local Similarity 26.9%; Pred. No. 1.5e+02;
Matches 7; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 2 AEFPHDSGYEVHOKLVEFADVGSN 27
|:|:|:|:|:
DB 213 ANYSLSLYRBERERIAFYEDIGLN 238

RESULT 60
A60999
alpha-amylose (EC 3.2.1.1) precursor - Micrococcus sp. (strain 207)
C/Species: Micrococcus sp.
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A60999
R/Kimura, T.; Horikoshi, K.
FEBS Microbiol. Lett. 71, 35-42, 1990
A/Title: The nucleotide sequence of an alpha-amylose gene from an alkalophytotrophic M
A/Reference number: A60999
A/Accession: A60999
A/Molecule type: DNA
A/Residues: 1-1104 <KIM>
A/Cross-references: UNIPROT:Q06812; UNIPARC:UPI00000BCA94; GB:X55799; NID:G296762; PIDN:
C/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycosyl/starch degradation
C/Superfamily: pullulanase type debranching enzyme
A/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/1-32/Domains: signal sequence #status predicted <SIG>
F/33-1104/Product: alpha-amylose #status predicted <MAT>

Query Match 27.8%; Score 45; DB 2; Length 1104;
Best Local Similarity 36.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 6 HDSGYEVHOKLVEFADV 24
||:|||||:
DB 182 HEMTEPERNERVFLANDI 200

RESULT 61
AB1847
serine/threonine kinase with two-component sensor domain all0323 [imported] - Nostoc sp.
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AB1847
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi,
N.; Shimizu, S.; Sugimoto, M.; Takasawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 6, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A/Reference number: AB1807; MUID:21595285; PMID:11759640
A/Accession: AB1847
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1808 <KUR>
A/Cross-references: UNIPROT:Q8Y2Y1; UNIPARC:UPI00000CDCB8; GB:BA000019; PIDN:BA872281.1
C/Genetics:
A/Genome: all0323

Query Match 27.8%; Score 45; DB 2; Length 1808;
Best Local Similarity 53.3%; Pred. No. 4.4e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 11 EVHOKLVEFADV 25
||:|||||:
DB 78 EHHKRLVLEFEDFG 92

RESULT 62
AE1302
probable phosphoprotein phosphatase homolog lmo1821 [imported] - Listeria monocytogenes
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AE1302
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fehl, H
Science 294, 849-852, 2001
A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AE1302
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-252 <GLA>
A/Cross-references: UNIPROT:Q8Y678; UNIPARC:UPI0000054E16; GB:NC_003210; PIDN:CAC99899.
A/Experimental source: strain BGD-e
C/Genetics: lmo1821
A/Genome: lmo1821

Query Match 27.5%; Score 44.5; DB 2; Length 252;
Best Local Similarity 30.0%; Pred. No. 59;
Matches 12; Conservative 5; Mismatches 10; Indels 13; Gaps 1;

QY 2 AEFPHDSGYEVH-----OKLVEFADVGSNK 28
||:|||||:
DB 3 AEFPHDSGRIRHNEHNGVFNKNDPPIYVADSGMGR 42

RESULT 63
AE1674
probable phosphoprotein phosphatase homolog lin1935 [imported] - Listeria innocua (ecra
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AE1674
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fehl, H
Science 294, 849-852, 2001
A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AE1674
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-252 <GLA>
A/Cross-references: UNIPROT:Q92A17; UNIPARC:UPI00000CC6E5; GB:AU592022; PIDN:CAC97165.1
A/Experimental source: strain Clp11262

C:Genetics:
A:Gene: 11n1935
C:Superfamily: conserved hypothetical protein y100; conserved hypothetical protein y100

Query Match 27.5%; Score 44.5; DB 2; Length 252;
Best Local Similarity 30.0%; Pred. No. 59;
Matches 12; Conservative 5; Mismatches 10; Indels 13; Gaps 1;

OY 2 AEFRHDSGYEVH-----QKLVFPAEDVGSNK 28
DB 3 AEFRTRDGRIRRHNEEDNGVFNKDKPIYIVADMGGR 42

RESULT 64

hypothetical protein F19B15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T08962

R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16519

A:Accession: T08962

A:Molecule type: DNA

A:Residues: 1-317 <BEV>

A:Cross-references: UNIPROT:Q9SZD7; UNIPARC:UPI00009C9EB; EMBL:AL078470; GSPDB:GN00062;

A:Experimental source: cultivar Columbia; BAC clone F19B15

C:Genetics:

A:Gene: ATSP:F19B15.100

A:Map position: 4

A:Introns: 26/3; 244/1

C:Superfamily: Arabidopsis thaliana hypothetical protein F19B15.100

Query Match 27.5%; Score 44.5; DB 2; Length 317;
Best Local Similarity 39.3%; Pred. No. 76;
Matches 11; Conservative 3; Mismatches 9; Indels 5; Gaps 1;

OY 6 HDSGYEVHOKLVF-----FAEDVGSNK 28
DB 196 HDIGYDTHQAEILKADMAFLECLGSNK 223

RESULT 65

hypothetical protein C40H5.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19869

R:White, S.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19189

A:Accession: T19869

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-392 <WIL>

A:Cross-references: UNIPROT:Q9UW7; UNIPARC:UPI000007A940; EMBL:Z81482; PIDD:CA03955.2;

A:Experimental source: clone C40H5

C:Genetics:

A:Gene: CESP:C40H5.4

A:Map position: X

A:Introns: 35/1; 54/2; 117/1; 167/1; 207/2; 282/1; 323/3

Query Match 27.5%; Score 44.5; DB 2; Length 392;
Best Local Similarity 33.3%; Pred. No. 96;
Matches 9; Conservative 5; Mismatches 4; Indels 9; Gaps 1;

OY 1 DAEFRHDSGYEVHOKLVFPAEDVGSN 27
DB 327 EKDFFHELGIVLHH-----VGN 344

Query Match 27.5%; Score 44.5; DB 2; Length 392;
Best Local Similarity 33.3%; Pred. No. 96;
Matches 9; Conservative 5; Mismatches 4; Indels 9; Gaps 1;

OY 1 DAEFRHDSGYEVHOKLVFPAEDVGSN 27
DB 327 EKDFFHELGIVLHH-----VGN 344

RESULT 66

A69662

UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: A69662

R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Bert,

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; C

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eittington, J.; Fabret, C.; Ferrari, B

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gall

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.

Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinot,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon

A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyam

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida,

A:Authors: Yoshikawa, H.F.; Zumeit, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: A69662

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-436 <KUN>

A:Cross-references: UNIPROT:P70965; UNIPARC:UPI000060BA0; GB:Z99122; GB:AL009126; NID

A:Experimental source: strain 168

C:Genetics:

A:Gene: murA

C:Superfamily: UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurZ

Query Match 27.5%; Score 44.5; DB 2; Length 436;
Best Local Similarity 43.5%; Pred. No. 11e+02;
Matches 10; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

OY 3 EFRHDSGYEVHOKLVFPAEDV 24
DB 392 EKHHDGRYVDFHQKALGADI 414

OY 3 EFRHDSGYEVHOKLVFPAEDV 24
DB 392 EKHHDGRYVDFHQKALGADI 414

RESULT 67

hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: Columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C:Accession: F71420

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Di

P.; Wedler, H.; Wedler, E.; Wambut, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Gic

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomene

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; A

C.; Chalmers, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis th

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: F71420

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-559 <BEV>

A:Cross-references: UNIPROT:O23409; UNIPARC:UPI00000A75B8; GB:Z97339; NID:q2244901; PII

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 27.5%; Score 44.5; DB 2; Length 559;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 2 AEFRHDSGYEVHOKLV 18
DB 222 AQRADPGYEDYHRKFV 239

OY 2 AEFRHDSGYEVHOKLV 18
DB 222 AQRADPGYEDYHRKFV 239

RESULT 68

C91683
3-methyl-2-oxobutanate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain TC061
N:Alternate names: oxoalvalerate dehydrogenase
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C91683
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: C91683
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-678 <TEXT>
A:Cross-references: UNIPROT:Q9PK54, UNIPARC:UPI00000579C3, GB:AEO02330, GB:AEO02160, NID
A:Experimental source: strain N199 (Mopn)
C:Genetics:
A:Gene: TC0618
C:Keywords: oxidoreductase
Query Match 27.5%; Score 44.5; DB 2; Length 678;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
OY 11 EVHHOK-LVFAEDVGSNKG 29
DB 364 EHHRDGVVFGEDVAGNKG 383
RESULT 69
T36143
probable secreted proteinase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2003
C:Accession: T36143
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T36143
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-781 <SER>
A:Cross-references: UNIPARC:UPI000000DB27A; EMBL:AL096852; PIDD:CAM51001.1; GSPDB:GN00070
A:Experimental source: strain A3(12)
C:Genetics:
A:Gene: SCODB:SCB19A.20C
C:Superfamily: secreted virulence protease, TmbA type
Query Match 27.5%; Score 44.5; DB 2; Length 781;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 10; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKG 30
DB 261 DGFNEPDGY-IDHFOIVHAGEDSAGGA 289
RESULT 70
A55734
sodium channel, voltage-gated, beta-1 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55734; A53408; I54354
R:Markita, N.; Sloan-Brown, K.; Weghuis, D.O.; Roper, H.H.; George Jr., A.L.
Genomics 23, 628-634, 1994
A:Title: Genomic organization and chromosomal assignment of the human voltage-gated Na(+)
A:Reference number: A55734; MUID:95154833; PMID:7851891
A:Accession: A55734
A:Molecule type: DNA
A:Residues: 1-218 <MAX>
A:Cross-references: UNIPROT:Q07699; UNIPARC:UPI00000532B2; GB:U12189
R:Markita, N.; Bennett Jr., P.B.; George Jr., A.L.

J. Biol. Chem. 269, 7571-7578, 1994
A:Title: Voltage-gated Na(+) channel beta-1 subunit mRNA expressed in adult human skele
A:Reference number: A53408; MUID:941171787; PMID:8125980
A:Accession: A53408
A:Molecule type: mRNA
A:Residues: 1-218 <MAX>
A:Cross-references: UNIPARC:UPI00000532B2; GB:U16242; NID:9450602; PIDD:AAA61277.1; PID
R:Markita, N.; Sloan-Brown, K.; Weghuis, D.O.; Roper, H.H.; George Jr., A.L.
Genomics 23, 628-634, 1994
A:Title: Genomic organization and chromosomal assignment of the human voltage-gated Na(+)
A:Reference number: A53408; MUID:95154833; PMID:7851891
A:Accession: A53408
A:Molecule type: DNA
A:Residues: 1-218 <MAX>
A:Cross-references: UNIPARC:UPI00000532B2; GB:U10338; NID:9307414; PIDD:AAA60391.1; PID
C:Genetics:
A:Gene: GDB:SCN1B
A:Cross-references: GDB:127281; OMIM:600235
A:Map position: 19q13.1-19q13.1
C:Keywords: glycoprotein; muscle; transmembrane protein
F.1-19/Dominant: signal sequence #status predicted <Sig>
F.161-182/Dominant: transmembrane #status predicted <TM>
F.193,110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 27.2%; Score 44; DB 2; Length 218;
Best Local Similarity 41.2%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
OY 4 FRHDSGYEVHOKLVFP 20
DB 113 YNHSGDYECVYRLFF 129
RESULT 71
A42737
sodium channel beta 1 subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42737
R:Riosom, L.V.; De Jongh, K.S.; Patton, D.E.; Reber, B.F.; Offord, J.; Charbonneau, H.; W
Science 256, 839-842, 1992
A:Title: Primary structure and functional expression of the beta 1 subunit of the rat b
A:Reference number: A42737; MUID:92271207; PMID:1375395
A:Accession: A42737
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-218 <ISO>
A:Cross-references: UNIPROT:Q00954; UNIPARC:UPI00000341E5; GB:M91808; NID:G206864; PIDN
A:Experimental source: brain
C:Keywords: transmembrane protein
Query Match 27.2%; Score 44; DB 2; Length 218;
Best Local Similarity 41.2%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
OY 4 FRHDSGYEVHOKLVFP 20
DB 113 YNHSGDYECVYRLFF 129
RESULT 72
A4978
hypothetical protein b2106 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A4978
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A4978; MUID:97426617; PMID:9278503

A:Accession: A64978
A:Status: preliminary, nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-274 <BLAT>
A:Cross-references: UNIPROT:P76425; UNIPARC:UPI000003EAD4; GB:AE000299; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain MG1655

Query Match 27.2%; Score 44; DB 2; Length 274;
Best Local Similarity 46.7%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DAERHDSGYEVMHQ 15
Db 131 DHEHHDHGHHHHH 145

RESULT 73
S04278
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni)
N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
C:Species: Schistosoma mansoni
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-2004
C:Accession: S04278; S01201
R:Craig, S.P.; Muralidhar, M.G.; McKerrow, J.H.; Wang, C.C.
submitted to the EMBL Data Library, November 1988
A:Reference number: S04278
A:Accession: S04278
A:Molecule type: DNA
A:Residues: 1-284 <CRA>
A:Cross-references: UNIPROT:P09383; UNIPARC:UPI000012CB6B; EMBL:X13531; NID:g10181; PIDN
R:Craig III, S.P.; McKerrow, J.H.; Newport, G.R.; Wang, C.C.
Nucleic Acids Res. 16, 7087-7101, 1988
A:Title: Analysis of cDNA encoding the hypoxanthine-guanine phosphoribosyltransferase (H
A:Reference number: S01201; MUID:86303331; PMID:3136439
A:Accession: S01201
A:Molecule type: mRNA
A:Residues: 1-231 <CRA2>
A:Cross-references: UNIPARC:UPI0000175408; EMBL:X07883
C:Genetics: 66/3; 102/3; 166/3; 188/3; 221/3; 237/3; 262/3
A:introns: 66/3; 102/3; 166/3; 188/3; 221/3; 237/3; 262/3
C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 27.2%; Score 44; DB 2; Length 284;
Best Local Similarity 36.0%; Pred. No. 80;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 3 EFRHDSGYEVMHQKLVFPAEDVGSN 27
Db 233 DYRDVGFEVNRFRVGVGLDYNDN 257

RESULT 74
S29599
acrosin (EC 3.4.21.10) precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S29599
R:Gerton, G.L.; Hoff, H.B.; Baba, T.
submitted to the EMBL Data Library, May 1992
A:Description: The amino acid sequence of guinea pig proacrosin deduced from its cDNA se
A:Reference number: S29599
A:Accession: S29599
A:Molecule type: mRNA
A:Residues: 1-421 <GER>
A:Cross-references: UNIPROT:Q60491; UNIPARC:UPI000005C67; EMBL:Z12153; NID:g49559; PIDN
C:Superfamily: acrosin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:41-284/Domain: trypsin homology <TRY>

Query Match 27.2%; Score 44; DB 2; Length 421;
Best Local Similarity 45.8%; Pred. No. 1.2e+02;
Matches 11; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

Qy 7 DSGYEVHMQKLVFPAEDV--GSNK 28
Db 90 DSKKKVYDMLVFCFAEIEYGNKK 113

RESULT 75
AB2427
hypothetical protein al14970 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <KIR>
A:Cross-references: UNIPROT:Q8YMG4; UNIPARC:UPI00000CECF9; GB:BA000019; PIDN:BA076665.1
A:Experimental source: strain PCC 7120
C:Genetics: 6
A:Gene: al14970

Query Match 27.2%; Score 44; DB 2; Length 698;
Best Local Similarity 30.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 6 HDSGYEVHMQKLVFPAEDVG 25
Db 186 HSDRYPIHEQVAGINQEIIG 205

RESULT 76
C86268
F13B4.2 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86268
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, N.F.; Hughes, B.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.K.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Mailli, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86268
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-702 <STO>
A:Cross-references: UNIPROT:Q9FZ73; UNIPARC:UPI00000A95C4; GB:AE005172; NID:g9802751; P
C:Genetics: 1
A:Map position: 1

Query Match 27.2%; Score 44; DB 2; Length 702;
Best Local Similarity 72.7%; Pred. No. 2.2e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 18 VFPAEDVGSNK 28
Db 566 VFPCENYGNKK 576

RESULT 77
PABVBS
alpha-a protein - barley stripe mosaic virus
C:Species: barley stripe mosaic virus, BSMV

A/Note: host Hordeum vulgare (barley)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: JA0109; FN0104
R/Guestion, G.; Armur, S.L.; Gamboa, G.C.; Burgett, S.G.; Shepherd, J.W.
V/ology 170, 370-377, 1989
A/Title: Nucleotide sequence of barley stripe mosaic virus RNA alpha: RNA alpha encodes
A/Reference number: JA0109; MUID:9268457; PMID:2728343
A/Accession: JA0109
A/Molecule type: genomic RNA
A/Residues: 1-1139 <GUS>
A/Cross-references: UNIPROT:P17595; UNIPARC:UPI0000138D67; GB:J04342; NID:G331510; PIDN:
R/Kozlov, Y.V.; Afanasiev, B.N.; Rupasov, V.V.; Golova, Y.B.; Kulaseva, O.I.; Dolja, V.V.
Mol. Biol. (Mosk.) 23, 1080-1090, 1989
A/Title: The complete nucleotide sequence of barley stripe mosaic virus RNA 3 and its va
A/Reference number: FN0102; MUID:90066400; PMID:2586501
A/Accession: FN0104
A/Molecule type: genomic RNA
A/Residues: 935-941, 'E', 943-976, 'R', 978-997, 'L', 999-1006, 'F', 1008-1056, 'L', 1058-1129, 'L'
A/Cross-references: UNIPARC:UPI00000F324C
A/Note: the authors translated the codon GAA for residue 942 as Gln and CCC for residue
C/Genetics:
A/Map position: segment 1
C/Superfamily: barley stripe mosaic virus alpha-a protein

Query Match 27.2%; Score 44; DB 1; Length 1139;
Best Local Similarity 28.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 4 FRHDSGYEVHOKLVFPAEDVSNK 28
Db 909 FHPDEALKVYGAIMFCADKLGASE 933

RESULT 78
S48420
probable membrane protein YIL059C - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C/Accession: S48420
R/Smith, V.
submitted to the EMBL Data Library, September 1994
A/Reference number: S48407
A/Accession: S48420
A/Molecule type: DNA
A/Residues: 1-121 <SMT>
A/Cross-references: UNIPROT:P40520; UNIPARC:UPI000013B3D6; GB:Z47047; EMBL:Z38060; NID:G
C/Genetics:
A/Gene: MIPS:YIL059C
A/Cross-references: SGD:S0001321
A/Map position: 9L
C/Superfamily: Saccharomyces probable membrane protein YIL059C
C/Keywords: transmembrane protein
F/6-22/Domain: transmembrane #status predicted <TM>

Query Match 26.9%; Score 43.5; DB 2; Length 121;
Best Local Similarity 35.5%; Pred. No. 37;
Matches 11; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

Qy 2 AEFHDSGYEVH--HOKLVFPAEDVSNK 29
Db 23 AEFDFDVGEEFVNTPTFLSDIGLHV 53

RESULT 79
T13179
hypothetical protein I143 - Lactobacillus phage phi-gle
C/Species: Lactobacillus phage phi-gle
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C/Accession: T13179
R/Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taketo,
Gene 187, 45-53, 1997
A/Title: Genome structure of the lactobacillus temperate phage phi gle: the whole genome
A/Reference number: Z17631; MUID:97225795; PMID:9073065

A/Accession: T13179
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-143 <KOD>
A/Cross-references: UNIPARC:UPI000009B29A; EMBL:X98106; NID:G1926320; PIDN:CAA6783.1; F
C/Genetics:
A/Note: Lorf143
C/Superfamily: Lactobacillus phage phi-gle hypothetical protein I143

Query Match 26.9%; Score 43.5; DB 2; Length 143;
Best Local Similarity 42.9%; Pred. No. 44;
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;

Qy 9 GYEVHOKLVFPAEDVSNK 29
Db 29 GFEVHF-----EDIGANWG 42

RESULT 80
T21923
hypothetical protein F37H8.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T21923
R/Gregory, J.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19488
A/Accession: T21923
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-284 <WIL>
A/Cross-references: UNIPROT:O17862; UNIPARC:UPI000007D023; EMBL:Z81534; PIDN:CAR04346.1,
A/Experimental source: clone F37H8
C/Genetics:
A/Gene: CRSP:F37H8.1
A/Map position: 2
A/Intons: 23/3; 81/2; 132/2; 168/3; 257/2

Query Match 26.9%; Score 43.5; DB 2; Length 284;
Best Local Similarity 58.8%; Pred. No. 94;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 3 EFRHDSGYEVHOKLVF 19
Db 69 EFRH--SPFYHOKLVF 84

RESULT 81
A13443
Na+/H+ antiporter 1 / proteinase IV (EC 3.4.-.-) [imported] - Brucella melitensis (strai
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: A13443
R/DeIvecchio, V.G.; Kapactral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melite
A/Reference number: AD3252; PMID:11756688
A/Accession: A13443
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-763 <KUR>
A/Cross-references: UNIPROT:Q6YF15; UNIPARC:UPI0000580B5; GB:AE008917; PIDN:PAL52716.1
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME11535
A/Map position: I
C/Superfamily: Na(+)/H(+) antiporter 1/protease IV-related
C/Keywords: hydrolase

Query Match 26.9%; Score 43.5; DB 2; Length 763;
Best Local Similarity 40.7%; Pred. No. 2.8e+02;

Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Query 4 FRHDSGYEVHOKLVF-FAEDVGSNKG 29
 Db 552 YKRIRDLAAEHOKKVFVFDVAASG 578

RESULT 82
 T05068
 hypothetical protein M3B9.210 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T05068
 R/Beyan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hebeisel, J.; Mewes, H.W.; Mayer
 submitted to the Protein Sequence Database, March 1999
 A/Reference number: Z15396
 A/Accession: T05068
 A/Molecule type: DNA
 A/Residues: 1-1141 <BBV>
 A/Cross-references: UNIPROT:O65598; UNIPARC:UPI00000A4AD7; EMBL:AL022223
 A/Experimental source: cultivar Columbia; BAC clone M3B9
 C/Genetics:
 A/Map position: 4
 A/Intons: 463/3; 885/1; 1081/2
 A/Note: M3B9.210

Query Match 26.9%; Score 43.5; DB 2; Length 1141;
 Best Local Similarity 40.7%; Pred. No. 4.4e+02;
 Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 1;

Query 5 RHDSGYEVHOKLVF-FAEDV 24
 Db 653 RFDGTYRHPKASDLSTHMFADV 679

RESULT 83
 F70435
 glutamate synthase (ferredoxin) (EC 1.4.7.1) precursor [similarity] - Aquifex aeolicus
 C/Species: Aquifex aeolicus
 C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
 C/Accession: F70435
 R/Dackert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
 V.
 Nature 392, 353-358, 1998
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A/Reference number: A70300; MUID:98196666; PMID:9537320
 A/Accession: F70435
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-1493 <AOF>
 A/Cross-references: UNIPROT:O67512; UNIPARC:UPI000005665F; GB:AE000746; NID:q2983925; PI
 A/Experimental source: strain VF5
 C/Genetics:
 A/Gene: gltB
 C/Superfamily: glutamate synthase, large subunit
 C/Keywords: 3fe-4S; metalloprotein; oxidoreductase
 F/1-7/Domain: propeptide #status predicted <PRO>
 F/8-1493/Product: glutamate synthase #status predicted <MAY>
 F/8/Active site: Cys #status predicted
 F/117,1123,1128/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 26.9%; Score 43.5; DB 2; Length 1493;
 Best Local Similarity 38.5%; Pred. No. 5.9e+02;
 Matches 10; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

Query 5 RHDSGYEVHOKLVF-FAEDVGSNKA 30
 Db 782 RHNAAYVEERKL-----DIGHMK 802

RESULT 84
 F69770
 hypothetical protein ydbC - Bacillus subtilis

C/Species: Bacillus subtilis
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C/Accession: F69770
 R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E
 Nature 390, 249-256, 1997
 A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holst, M.; Holst, S.; Hullo, M.F
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin
 A/Authors: Lauder, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
 Riger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
 A/Authors: Schlecht, S.; Schreier, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Ser
 akenchi, M.; Tamakoshi, A.; Tanaka, T.; Terpe, P.; Tognoni, K.; Tosa, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A/Authors: Yoshikawa, H.F.; Zumbach, E.; Yoshikawa, H.; Zumbach, A.
 A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A/Reference number: A69580; MUID:98044033; PMID:9384377
 A/Accession: F69770
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-119 <KUN>
 A/Cross-references: UNIPROT:P96598; UNIPARC:UPI000005FF5C; GB:Z99106; GB:AL009126; NID:
 A/Experimental source: strain 168
 C/Genetics:
 A/Gene: ydbC

Query Match 26.5%; Score 43; DB 2; Length 119;
 Best Local Similarity 45.5%; Pred. No. 43;
 Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Query 3 EFRHDSGYEVHOKLVF-FAEDV 24
 Db 68 ENEHDSYEVHOKLVF-FAEDV 89

RESULT 85
 JC7732
 trypsin-plasmin inhibitor, bdellin-KL - Korean leech
 C/Species: Hirudo nippona (Korean leech)
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C/Accession: JC7732
 R/Kim, Y.H.; Choi, J.G.; Lee, G.M.; Kang, K.W.
 J. Biochem. 130, 431-438, 2001
 A/Title: Domain and genomic sequence analysis of bdellin-KL, a leech-derived trypsin-pl
 A/Reference number: JC7732; MUID:21421308; PMID:11530020
 A/Accession: JC7732
 A/Molecule type: mRNA
 A/Residues: 1-155 <KIM>
 A/Cross-references: UNIPROT:Q9NCC2; UNIPARC:UPI0000074PF58; GB:AF223972; GB:AF22790
 C/Comment: This protein is a novel bifunctional inhibitor with two distinct domains. Wh
 ing region for charged molecules.

Query Match 26.5%; Score 43; DB 2; Length 155;
 Best Local Similarity 60.0%; Pred. No. 57;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query 6 HDGSGYEVHOKLVF-FAEDV 15
 Db 87 HDGSGYEVHOKLVF-FAEDV 96

RESULT 86
 S74834
 hypothetical protein s110854 - Synecocystis sp. (strain PCC 6803)
 C/Species: Synecocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S74834
 R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asami, E.; Nakamura, Y.; Miyajima, N.
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaed
 DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
8.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S74814
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1308 <RNA>
A/Cross-references: UNIPROT:P73746; UNIPARC:UP100000C0D8E; EMBL:D90909; GB:AB01339; NID
C/Note: the nucleotide sequence was submitted to the EMBL data library, June 1996
C/Superfamily: *Synechocystis* hypothetical protein s110854

Query Match 26.5%; Score 43; DB 2; Length 308;
Best Local Similarity 42.3%; Pred. No. 1.2e+02;
Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 2;

QY 2 AERFHDGGR-EVHOK--LVFPAEDV 23
Db 262 SQVRHDCAYLEIPHSYLLVFTEN 287

RESULT 87
A81351
Signal transduction histidine kinase Cj0793 [imported] - *Campylobacter jejuni* (strain NC
C/Species: *Campylobacter jejuni*
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: A81351
R/Authors: Kreft, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrett
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyf
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Accession: A81351
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-339 <PAR>
A/Cross-references: UNIPROT:Q9PP6C; UNIPARC:UP100000C1D36; GB:AL139076; GB:AL111168; NID
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Supfamily: Cj0793

Query Match 26.5%; Score 43; DB 2; Length 339;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 6 HDGGEVHOKLVFPAEDVGSNKG 29
Db 281 YDNGCEIKDKLVFPAEKTKTKMG 304

RESULT 88
AD1201
N-acetyl-L-amino acid amidohydrolases homolog lmo1012 [imported] - *Listeria monocytogenes*
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C/Accession: AD1201
R/Authors: F.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; Ma
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AD1201
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-371 <GUA>
A/Cross-references: UNIPROT:Q8Y8A0; UNIPARC:UP100000C1F129; GB:NC_003210; PIDN:CAC99090.1
A/Experimental source: strain EGD-e
C/Genetics:
A/Supfamily: Hipurate hydrolase

Query Match 26.5%; Score 43; DB 2; Length 371;
Best Local Similarity 45.8%; Pred. No. 1.5e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 6; Gaps 1;

QY 7 DSGEYVHOKL-----VFPADV 24
Db 340 DSEYSLHAKLSPKEAIPFADIV 363

RESULT 89
AB1559
N-acetyl-L-amino acid amidohydrolases homolog lml1011 [imported] - *Listeria innocua* (stra
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C/Accession: AB1559
R/Authors: Kreft, J.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AB1559
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-371 <GUA>
A/Cross-references: UNIPROT:Q92D10; UNIPARC:UP100000C41F; GB:AL592022; PIDN:CAC96242.1
A/Experimental source: strain Clp11262
C/Genetics:
A/Supfamily: Hipurate hydrolase

Query Match 26.5%; Score 43; DB 2; Length 371;
Best Local Similarity 45.8%; Pred. No. 1.5e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 6; Gaps 1;

QY 7 DSGEYVHOKL-----VFPADV 24
Db 340 DSEYSLHAKLSPKEAIPFADIV 363

RESULT 90
B86268
F13B4.1 protein - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86268
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.P.; Hubbard, B.; Hultizer, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
A.; Liu, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maitl, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.W.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: AB6141; MUID:21016719; PMID:11130712
A/Accession: B86268
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-382 <STO>
A/Cross-references: UNIPROT:Q9F74; UNIPARC:UP100000A5523; GB:AE005172; NID:G9802750; P
A/Genetics:
A/Map position: 1

Query Match 26.5%; Score 43; DB 2; Length 382;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 18 VFPAEDVGSNK 28
||| |::|

Db 247 VFECENIGNNK 257

RESULT 91

A:Title: hypothetical protein Vng1057c [imported] - Halobacterium sp. NRC-1
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70940
A:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84262
R:NG, W.V.; Kennedy, S.P.; Mahairae, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Lettner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Uabid Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: A84262
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <STO>
A:Cross-references: UNIPROT:Q9HQ02; UNIPARC:UPI00000637D3; GB:AE004437; NID:g10580605; F
C:Genetic8:
A:Gene: VNG1057C

Query Match 26.5%; Score 43; DB 2; Length 452;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVH 13
Db 76 AELRDSGYETH 87

RESULT 92

A49388
A:Title: catalase (BC 1.11.1.6), sialic acid-binding - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 04-Mar-2000
C:Accession: A49388
R:Chen, Z.; Silva, H.; Klessig, D.F.
Science 262, 1883-1886, 1993
A:Title: Active oxygen species in the induction of plant systemic acquired resistance by
A:Reference number: A49388; MUID:94090318; PMID:8266079
A:Accession: A49388
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-489 <CHE>
A:Cross-references: UNIPARC:UPI000016DE70; GB:U03473; NID:g436477; PIDN:AMC48918.1; PID:
C:Superfamily: catalase
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:62,101,135/Active site: His, Ser, Asn #status predicted
F:345/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 26.5%; Score 43; DB 2; Length 489;
Best Local Similarity 43.8%; Pred. No. 2e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHOKLV 18
Db 195 DYRHEGYGVHAYOLI 210

RESULT 93

C70940
A:Title: probable cobQ protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70940
R:Cole, S.T.; Broech, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Nature 393, 537-544, 1998
A:Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, .; Taylor, K.; Whitehead, S.; Barrett, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70940
A:Species: Catharantus roseus (Madagascar periwinkle)
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-494 <COL>
A:Cross-references: UNIPROT:O53677; UNIPARC:UPI0000127DF9; GB:AL021929; GB:AL123456; NJ
A:Experimental source: strain H37RV
C:Genetic8:
A:Gene: cobQ
C:Superfamily: probable cobQ acid synthase

Query Match 26.5%; Score 43; DB 2; Length 494;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 SGYEVHOKLV 17
Db 391 SGYEVHGR 400

RESULT 94

T10000
A:Title: cytochrome P450 (CYP72C) - Madagascar periwinkle (fragment)
C:Species: Catharantus roseus (Madagascar periwinkle)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C:Accession: T10000
R:Mangold, U.; Riebel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck
Plant Sci. 96, 129-136, 1994
A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharant
A:Reference number: Z16915
A:Accession: T10000
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-516 <MAN>
A:Cross-references: UNIPROT:Q42701; UNIPARC:UPI0000042837; EMBL:L19075; NID:g404689; P1
A:Experimental source: cv. cp3
C:Genetic8:
A:Gene: CYP72C
C:Keywords: heme; iron; metalloprotein
F:318-461/domain: cytochrome P450 homology <P45-
F:45/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 26.5%; Score 43; DB 2; Length 516;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 5 RHDSGYEVHOKLVPAEDVSNKGA 30
Db 115 KYQKNFVHNPVIVFLTVGSPFGA 140

RESULT 95

T09999
A:Title: cytochrome P450 - Madagascar periwinkle
C:Species: Catharantus roseus (Madagascar periwinkle)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09999
R:Mangold, U.; Riebel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck
Plant Sci. 96, 129-136, 1994
A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharant
A:Reference number: Z16915
A:Accession: T09999
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <MAN>
A:Cross-references: UNIPROT:Q42700; UNIPARC:UPI000004B88E; EMBL:L19074; NID:g404687; P1
A:Experimental source: cv. cp3
C:Genetic8:
A:Gene: CYP72B
A:Introns: 96/1; 170/3; 252/2; 381/3
C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein

F:329-492/Domain: cytochrome P450 homology <P45>
F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 26.5%; Score 43; DB 2; Length 524;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 5 RHDSGYEVHHQKLVFPADVGSNKA 30
Db 126 KYQKMFVHNPLVYFLLTGVGSFEGA 151

RESULT 96
T09944
Probable cytochrome P450 protein - Madagascar periwinkle
N/Alternate names: CYP72 protein
C/Species: Catharanthus roseus (Madagascar periwinkle)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09944
R/Author: H.P. Mangold, U. Schroeder, G. Marner, F.J. Werck-Reichhart, D. Schroeder
Plant Physiol 100, 998-1007, 1992
A/Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450
A/Reference number: Z16302
A/Accession: T09944
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-524 <VRT>
A/Cross-references: UNIPROT:Q05047, UNIPARC:UPI000012820D, EMBL:L10081, NID:9167483, PTD
C/Genetics:
A/Gene: CYP72
C/Superfamily: human cytochrome P450 CYP4B1, cytochrome P450 homology
C/Keywords: heme; iron; metalloprotein <P45>
F:319-492/Domain: cytochrome P450 homology <P45>
F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 26.5%; Score 43; DB 2; Length 524;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 5 RHDSGYEVHHQKLVFPADVGSNKA 30
Db 126 KYQKMFVHNPLVYFLLTGVGSFEGA 151

RESULT 97
E96786
Protein F10A5.13 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: E96786
R/Author: J. Ecker, J.R. Palm, C.J. Federipiel, N.A. Kaul, S. White, O. Alonso, Chin, C.W., Hughes, B.J. Hulzar, L.
Nature 408, 816-820, 2000
A/Title: The genome sequence of the plant Arabidopsis.
A/Reference number: A86141, MUID:21016719, PMID:11130712
A/Accession: E96786
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-525 <STO>
A/Cross-references: UNIPROT:Q9LR07, UNIPARC:UPI00000AC71F, GB:A8005173, NID:99369363; PTD
C/Genetics:
A/Gene: F10A5.13
A/Map position: 1
C/Superfamily: Arabidopsis membrane-anchored cellulase KOR

Query Match 26.5%; Score 43; DB 2; Length 525;
Best Local Similarity 36.4%; Pred. No. 2.2e+02;

Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 8 SGYEVHHQKLVFPADVGSNKG 29
Db 310 AGTYVLLSRLLFPKDLSSGSKG 331

RESULT 98
T45058
Phosphoprotein phosphatase (EC 3.1.3.16) Y39B6B.ff [similarity] - Caenorhabditis elegans
N/Alternate names: serine/threonine phosphatase pps homolog
C/Species: Caenorhabditis elegans
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 28-Apr-2003
C/Accession: T45058
R/Author: R. Almscough, R. Anderson, K. Baynes, C. Berke, M. Bonfield, J. Burton, Raser, A. Fulton, L. Gardner, A. Green, P. Hawkins, T. Hillier, L. Jier, M. John, B. O'Callaghan, M. Parsons, J. Percy, C. Rifkin, L. Roopra, A. Saunders, D. Nature 368, 32-38, 1994
A/Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A/Reference number: S43531, MUID:94150718, PMID:7906398
A/Accession: T45058
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-526 <MTL>
A/Cross-references: UNIPARC:UPI0000083436, EMBL:AL132896, NID:96434440, PTD:CA60937.1, A/Experimental source: clone Y39B6B
C/Genetics:
A/Map position: 3
A/Intons: 42/1, 124/3, 184/3, 265/3, 348/3, 385/2, 415/2, 499/3
A/Note: Y39B6B.ff
C/Superfamily: protein phosphatase 5; phosphoesterase core homology; phosphoprotein pho
C/Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc
F:29-61/Domain: tetratricopeptide repeat homology <TR1>
F:29-61/Domain: tetratricopeptide repeat homology <TR2>
F:62-95/Domain: tetratricopeptide repeat homology <TR3>
F:96-129/Domain: tetratricopeptide repeat homology <TR4>
F:203-497/Domain: phosphoprotein phosphatase homology <PPP>
F:235-304/Domain: phosphoesterase core homology <PEC>
F:241, 243, 270/Binding site: Iron (Asp, His, Asp) #status predicted
F:270, 302, 351, 456/Binding site: Zinc (Asp, Asn, His, His) #status predicted
F:273, 303, 480/Active site: Asp, His, Tyr #status predicted
F:274, 429/Binding site: substrate phosphate (Arg) #status predicted

Query Match 26.5%; Score 43; DB 1; Length 526;
Best Local Similarity 46.4%; Pred. No. 2.2e+02;
Matches 13; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

Qy 9 GYEVHHQK--LVFPADVGSNKA 30
Db 462 GYEVHHQKCFVFSAPNYCDQNNKGA 489

RESULT 99
A82834
Hypothetical protein XF0221 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: A82834
R/Author: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82815, MUID:20165717, PMID:10910347
A/Note: for a complete list of authors see reference number A5328 below
A/Accession: A82834
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-613 <SIM>
A/Cross-references: UNIPROT:Q9PG67, UNIPARC:UPI00000C2333, GB:A8003875, GB:A8003849, NID
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Artur, P.; Abreu, F.A.; Agencio, M.; Alvarenga, R.; Bioner, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, U.E.A.; Carraro, D.M.; Carter, J. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kielegger, J.E.; Kuramao, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0221

Query Match 26.5%; Score 43; DB 2; Length 613;
Best Local Similarity 30.8%; Pred. No. 2.6e+02;
Matches 8; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY 4 FRHDSGYEVHOKLVFFAEDVSNKG 29
Db 457 FRHAGYNAVYEGMALYERLKGNG 482

RESULT 100

S60385
Probable membrane protein YOL152w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein AOB629; hypothetical protein O0443
C:Species: Saccharomyces cerevisiae

C>Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60385; S66849; S57673

R:Casamayor, A.; Aldea, M.; Casas, C.; Herrero, E.; Gamo, F.J.; Lafuente, M.J.; Gancedo,
Yeast 11, 1281-1288, 1995

A>Title: DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome
A:Reference number: S60385; MUID:96132030; PMID:8553699

A:Accession: S60385
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-629 <CAS>

A:Cross-references: UNIPROT:Q12333; UNIPARC:UPI000012ABFA; EMBL:Z48239; NID:g1163073; PI
R:Atino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, C

submitted to the Protein Sequence Database, July 1996
A:Reference number: S66814

A:Accession: S66849
A:Molecule type: DNA

A:Residues: 1-629 <ARI>
A:Cross-references: UNIPARC:UPI000012ABFA; EMBL:Z74894; NID:g1420058; PTD:g

A:Experimental source: strain S288C
C:Genetics:

A:Gene: SGD:PRE7
A:Cross-references: SGD:S0005512; MIPS:YOL152w
A:Map position: 15L

C:Keywords: transmembrane protein
F:50-66/Domain: transmembrane #status predicted <TM1>

F:125-141/Domain: transmembrane #status predicted <TM2>
F:157-173/Domain: transmembrane #status predicted <TM3>

F:200-216/Domain: transmembrane #status predicted <TM4>
F:242-258/Domain: transmembrane #status predicted <TM5>

F:266-282/Domain: transmembrane #status predicted <TM6>
F:297-313/Domain: transmembrane #status predicted <TM7>

Query Match 26.5%; Score 43; DB 2; Length 629;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 RHDSGYEVHOK 16
Db 220 RHDSGYEVHOK 231

Search completed: April 20, 2006, 10:05:52
Job time : 43 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 20, 2006, 09:58:06 ; Search time 236 Seconds

(without alignments)
89.686 Million cell updates/sec

Title: US-10-666-423-1

Perfect score: 162
Sequence: 1 DAEPFHDSGEVHHQKLVFPAEDVGSNKGK 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	33	2	Q9UCJ3_HUMAN
2	162	100.0	42	2	Q56J06_GRAGR
3	162	100.0	42	2	Q56J07_TURTR
4	162	100.0	42	2	Q7M088_CAVPO
5	162	100.0	57	1	A4_URSWA
6	162	100.0	58	1	A4_CANFA
7	162	100.0	58	1	A4_RABIT
8	162	100.0	58	1	A4_SHEEP
9	162	100.0	59	1	A4_BOVIN
10	162	100.0	113	2	Q80H58_CHESE
11	162	100.0	534	2	Q93296_CHICK
12	162	100.0	569	2	Q9PVL1_CHICK
13	162	100.0	695	2	Q5R477_PONPY
14	162	100.0	695	2	Q5R477_PONPY
15	162	100.0	695	2	Q56J03_CANFA
16	162	100.0	695	2	Q56J03_CANFA
17	162	100.0	714	2	Q56J03_CANFA
18	162	100.0	749	2	Q56J03_CANFA
19	162	100.0	751	1	A4_SAISC
20	162	100.0	751	2	Q56J03_CANFA
21	162	100.0	751	2	Q56J03_CANFA
22	162	100.0	751	2	Q56J03_CANFA
23	162	100.0	751	2	Q56J03_CANFA
24	162	100.0	751	2	Q56J03_CANFA
25	162	100.0	770	1	A4_CANFA
26	162	100.0	770	1	A4_CANFA
27	162	100.0	770	1	A4_CANFA
28	162	100.0	770	1	A4_CANFA
29	162	100.0	770	1	A4_CANFA
30	162	100.0	770	1	A4_CANFA
31	162	100.0	770	2	Q56J06_CANFA

32	157	96.9	52	2	Q8W299_HUMAN	Q8W299 homo sapien
33	143	88.3	79	2	Q35463_CRIGR	Q35463 cricetus
34	143	88.3	218	2	Q8BPV5_MOUSE	Q8BPV5 mus musculu
35	143	88.3	384	2	Q8BPC7_MOUSE	Q8BPC7 mus musculu
36	143	88.3	693	2	Q8BSC0_XENLA	Q8BSC0 xenopus lae
37	143	88.3	695	2	Q6P6Q5_XAT	Q6P6Q5 rattus norv
38	143	88.3	733	2	Q6P6Q5_XAT	Q6P6Q5 rattus norv
39	143	88.3	747	2	Q91963_PIPPI	Q91963 xenopus lae
40	143	88.3	749	2	Q6NRRI_XENLA	Q6NRRI xenopus lae
41	143	88.3	750	2	Q6DJ06_XENTR	Q6DJ06 xenopus tro
42	143	88.3	770	1	A4_MOUSE	P13023 m amyloid b
43	143	88.3	770	1	A4_RAT	P08592 r amyloid b
44	143	88.3	770	2	Q532T3_MOUSE	Q532T3 mus musculu
45	143	88.3	770	2	Q547B7_RAT	Q547B7 rattus norv
46	140	86.4	695	2	Q98SF9_XENLA	Q98SF9 xenopus lae
47	140	86.4	695	2	Q7ZX00_XENLA	Q7ZX00 xenopus lae
48	133	82.1	699	2	Q57394_NARJA	Q57394 narke japon
49	120	74.1	754	2	Q4RY33_TETNG	Q4RY33 tetradon f
50	120	74.1	780	1	A4_TETFL	Q93279 fuigu rubrip
51	116	71.6	737	1	A4_FUGRU	Q480J4 tetradon n
52	116	71.6	759	2	Q480J4_TETNG	Q480J4 tetradon n
53	102.5	63.3	357	2	Q8UYR8_BRARE	Q8UYR8 brachydantio
54	102.5	63.3	472	2	Q8UYR8_BRARE	Q8UYR8 brachydantio
55	102.5	63.3	612	2	Q919E7_BRARE	Q919E7 brachydantio
56	102.5	63.3	678	2	Q7ZZT1_BRARE	Q7ZZT1 brachydantio
57	102.5	63.3	738	2	Q6NUZ1_BRARE	Q6NUZ1 brachydantio
58	102.5	63.3	738	2	Q90W28_BRARE	Q90W28 brachydantio
59	101	62.3	239	2	Q8UYU7_BRARE	Q8UYU7 brachydantio
60	101	62.3	362	2	Q8UYU7_BRARE	Q8UYU7 brachydantio
61	101	62.3	694	2	Q8UYU9_BRARE	Q8UYU9 brachydantio
62	66	40.7	49	2	Q7NGT4_BOVIN	Q7NGT4 boe taurus
63	59.5	36.7	545	2	Q7NGT4_GLOVI	Q7NGT4 globofacter
64	57	35.2	182	2	Q6EX80_PPOTV	Q6EX80 potato viru
65	57	35.2	327	1	POLG_PVYCH	P21294 potato viru
66	57	35.2	332	2	Q9D0N5_PPOTV	Q9D0N5 potato viru
67	57	35.2	337	2	Q8JPM2_PPOTV	Q8JPM2 potato viru
68	57	35.2	365	2	Q9WG05_PPOTV	Q9WG05 potato viru
69	55	34.0	182	2	Q6EX78_PPOTV	Q6EX78 potato viru
70	55	34.0	3063	1	POLG_PVYV	P18247 p genome po
71	55	34.0	3063	2	Q8J0O5_PPOTV	Q8J0O5 potato viru
72	54.5	33.6	687	2	Q56D14_ROMPA	Q56D14 romalea mtc
73	54	33.3	221	2	Q73UH3_MYCWA	Q73UH3 mycobacteri
74	54	33.3	284	1	POLG_PVYVO	P11897 potato viru
75	54	33.3	292	2	Q85276_PPOTV	Q85276 potato viru
76	53.5	32.7	971	1	V228_BOHRU	Q52662 arabidopsis
77	53	32.7	195	2	Q22662_ARATH	Q22662 arabidopsis
78	53	32.7	256	2	Q9CA59_ARATH	Q9CA59 arabidopsis
79	53	32.7	321	2	Q8RG41_FUSNN	Q8RG41 fusobacteri
80	53	32.7	339	2	Q7VDP1_PROMA	Q7VDP1 prochloroco
81	53	32.7	972	2	Q662D6_BORGA	Q662D6 borellia ga
82	53	32.7	1555	2	Q85274_PPOTV	Q85274 potato viru
83	52.5	32.4	324	2	Q5W16_LEGFL	Q5W16 legionella
84	52.5	32.4	324	2	Q5X504_LEGPA	Q5X504 legionella
85	52.5	32.4	939	2	Q52V81_LEGPH	Q52V81 legionella
86	52.5	32.4	939	2	Q52V81_LEGPH	Q52V81 legionella
87	52	32.1	182	2	Q6EX79_PPOTV	Q6EX79 potato viru
88	52	32.1	182	2	Q6EX81_PPOTV	Q6EX81 potato viru
89	52	32.1	256	2	Q7D5S5_MYCTU	Q7D5S5 mycobacteri
90	52	32.1	272	2	P66882_MYCTU	P66882 mycobacteri
91	52	32.1	272	2	Q7TWU2_MYCBO	Q7TWU2 mycobacteri
92	52	32.1	290	2	Q9EAB7_PPOTV	Q9EAB7 potato viru
93	52	32.1	290	2	Q9EAB8_PPOTV	Q9EAB8 potato viru
94	52	32.1	290	2	Q9EAD1_PPOTV	Q9EAD1 potato viru
95	52	32.1	698	2	Q9USK4_SPOLT	Q9USK4 spodoptera
96	51.5	31.8	3061	2	Q5ZPN7_PPOTV	Q5ZPN7 potato viru
97	51.5	31.8	199	2	Q8BYR3_MOUSE	Q8BYR3 mus musculu
98	51.5	31.8	321	2	Q63HM9_HUMAN	Q63HM9 homo sapien
99	51	31.5	328	2	Q9RPS4_ENTFA	Q9RPS4 enterococcu
100	51	31.5	344	2	Q41BK7_GIBZE	Q41BK7 gibberella

ALIGNMENTS

RESULT 1
Q9UC33 HUMAN PRELIMINARY; PRT; 33 AA.
ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE. PubMed=1406936; DOI=10.1038/359325a0;
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
RA Seubert P., Vigo-Pelfrey C., Esch P., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.,
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids."
RL Nature 359:325-327(1992).
DR HSSP; Q16019; 1BA4.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
Q56J06 GRAGR PRELIMINARY; PRT; 42 AA.
ID Q56J06 GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56J06 GRAGR PRELIMINARY; PRT; 42 AA.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.,
RT "The molecular machinery of Alzheimer's disease in the dolphin."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -, mRNA.
FT NON TER 1 42
FT NON TER 1 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30
DB 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30

RESULT 3
Q56J07 TURTR

ID Q56J07 TURTR PRELIMINARY; PRT; 42 AA.
AC Q56J07 TURTR PRELIMINARY; PRT; 42 AA.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Turstrops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Turstrops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.,
RT "The molecular machinery of Alzheimer's disease in the dolphin."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -, mRNA.
FT NON TER 1 42
FT NON TER 1 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30
DB 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30

RESULT 4
Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE. PubMed=7685598.
RX MEDLINE=93290653; PubMed=7685598.
RA Shimohiigashi Y., Matsunoto H., Takano Y., Saito R., Iwata T.,
RA Kamitaya H., Ohno M.,
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance P receptors."
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR HSSP; Q16019; 1IYT.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON TER 1 42
FT NON TER 1 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30
DB 1 DAERFHDGSEVHHQKLVFFAEDVGSNKG 30

RESULT 5
A4_URSMA

ID A4 URSA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalassiodromiidae).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae; Ursus.
CC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=2017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F; Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; X56128; CAA39593.1; -; mRNA.
DR PIR; B60045; B60045.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYL0ID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >57 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;
Query Match 100.0%; Score 162; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 30
DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 35
RESULT 6
A4_CANFA STANDARD; PRT; 58 AA.
ID_A4_CANFA
AC Q28280;

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
CC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=2017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F; Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56125; CAA39590.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR EMBL; ENSGAFG0000008557; Canis familiaris.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYL0ID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;
Query Match 100.0%; Score 162; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 30
DB 7 DAEFRHDSGYEVHHQKLVFFAEDVGNKGA 36
RESULT 7
A4_RABIT STANDARD; PRT; 58 AA.
ID_A4_RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```

DT 10-MAY-2005 (Rel. 47, last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE C-terminal fragment 40 (Beta-APP40); Gamma-Ctf(59) (Gamma-secretase
DE C-terminal fragment 59) (Gamma-Ctf(57) (Gamma-secretase C-terminal
DE fragment 57) (fragment)].
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083; SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Amyloid; Transmembrane.
KW AMYLOID; Transmembrane.
FT CHAIN <1 58
FT CHAIN 6 58
FT CHAIN 6 47
FT CHAIN 6 45
FT CHAIN 46 45
FT CHAIN 48 58
FT CHAIN 48 33
FT TOPO_DOM <1 33
FT TRANSMEM 34 57
FT TOPO_DOM 58 58
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 162; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 35

RESULT 8
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 10-MAY-2005 (Rel. 47, last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Soluble APP-

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DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-Ctf(59) (Gamma-secretase
DE C-terminal fragment 59) (Gamma-Ctf(57) (Gamma-secretase C-terminal
DE fragment 57) (fragment)].
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56130; CAA39595.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083; SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Amyloid; Transmembrane.
KW AMYLOID; Transmembrane.
FT CHAIN <1 58
FT CHAIN 6 58
FT CHAIN 6 47
FT CHAIN 6 45
FT CHAIN 46 45
FT CHAIN 48 58
FT CHAIN 48 33
FT TOPO_DOM <1 33
FT TRANSMEM 34 57
FT TOPO_DOM 58 58
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 162; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 30
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKG 35

RESULT 9
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 10-MAY-2005 (Rel. 47, last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-Ctf(59) (Gamma-secretase

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DE C-terminal fragment 59) ; Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57) ] (Fragment) .
GN Name=APP;
OS Bos taurus (Bovine) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos .
NCBI_TaxID=9913;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnson E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis." ;
RL Brain Res. Mol. Brain Res. 10:299-305(1991) .
CC -I- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(iO) (By similarity) .
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56124; CAA39589.1; -; mRNA.
DR EMBL; X56126; CAA39591.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; PTR01255; Beta-APP.
DR PANTHER; PTR010083; SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity) .
FT CHAIN 7 >59 CTF-alpha (By similarity) .
FT CHAIN 7 46 Beta-amyloid protein 42 (By similarity) .
FT CHAIN 7 48 Beta-amyloid protein 40 (By similarity) .
FT CHAIN 47 >59 Gamma-CTF(59) (By similarity) .
FT CHAIN 49 >59 Gamma-CTF(57) (By similarity) .
FT TOPO_DOM <1 34 Extracellular (Potential) .
FT TRANSMEM 35 58 Potential.
FT TOPO_DOM 59 >59 Cytoplasmic (Potential) .
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match 100.0%; Score 162; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGVEVHHQKLVFFAEDVGSNKA 30
DB 7 DAERFHDGVEVHHQKLVFFAEDVGSNKA 36

RESULT 10
Q8JH58_CHESE
ID Q8JH58_CHESE PRELIMINARY; PRT; 113 AA.
AC Q8JH58;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Amyloid beta protein (Fragment) .
OS Chelydra serpentina serpentina (common snapping turtle) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.

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OX NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876905; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina." ;
RL Environ. Health Perspect. 110:269-275(2002) .
DR EMBL; AF541917; AAN04908.1; -; mRNA.
DR HSSP; Q16019; 1IYT.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:Binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGVEVHHQKLVFFAEDVGSNKA 30
DB 15 DAERFHDGVEVHHQKLVFFAEDVGSNKA 44

RESULT 11
ID 093296_CHICK PRELIMINARY; PRT; 534 AA.
AC 093296;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Amyloid protein (Fragment) .
OS Gallus gallus (Chicken) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.B.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons." ;
RL J. Neurosci. 18:5869-5880(1998) .
DR EMBL; AF042098; AAC25052.1; -; mRNA.
DR HSSP; Q16019; 1IYT.
DR SMR; 093296; 224-333.
DR Ensembl; ENSGALG000000015770; Gallus gallus.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:Binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53BC2B66D4C92 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 436 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 465

RESULT 12
Q9PVL1_CHICK PRELIMINARY; PRT; 569 AA.
ID Q9PVL1_CHICK PRELIMINARY; PRT; 569 AA.
AC Q9PVL1; 13, Created
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, last annotation update)
DE Amyloid protein (Fragment).
DE Name=APP;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Brain;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -; mRNA.
DR HSSP; Q16019; IYIY.
DR SMR; Q9PVL1; 1-64, 260-369.
DR Ensembl; ENSGALG00000015770; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAMAMLOID.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB9BB851863A19D CRC64;

Query Match 100.0%; Score 162; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 472 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 501

RESULT 13
Q5R477_PONPY PRELIMINARY; PRT; 695 AA.
ID Q5R477_PONPY PRELIMINARY; PRT; 695 AA.
AC Q5R477; 29, Created
DT 01-FEB-2005 (TrEMBLrel. 29, last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, last annotation update)
DE Hypothetical protein DKFZ459D212.
GN Name=DKFZ459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Cortex;
RG The German CDNA Consortium;
Mambuti R., Heubner D., Mewes H.W., Well B., Amid C., Oeanger A.,

RA Pobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR61180; CA93459.1; -; mRNA.
DR SMR; Q5R477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:hemoglobin; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR012851; Beta-APP.
DR InterPro; IPR012852; Cytochrome_c_R.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAMAMLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Hypothetical protein.
SQ SEQUENCE 695 AA; 78626 MW; 0BF5D9BA2213E49 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 597 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 626

RESULT 14
Q6RH29_CANPA PRELIMINARY; PRT; 695 AA.
ID Q6RH29_CANPA PRELIMINARY; PRT; 695 AA.
AC Q6RH29; 27, Created
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Beta amyloid protein isoform APP695.
GN Name=Beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY498707; AAR97727.1; -; mRNA.
DR HSSP; Q16019; IEA4.
DR SMR; Q6RH29; 28-123, 124-189, 385-494.
DR Ensembl; ENSCARG00000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAMAMLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 718CA42A9F9B6C10 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30

Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 626

RESULT 15

056UK3_CANFA PRELIMINARY; PRT; 695 AA.
AC 056UK3;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY26582; AAX81911.1; -; mRNA.
SQ SEQUENCE 695 AA; 78748 MW; 5A253B0DB677875A CRC64;

Query Match 100.0%; Score 162; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 3,1e-15;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 30

Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 626

RESULT 16

09DGJ8_CHICK PRELIMINARY; PRT; 695 AA.
ID 09DGJ8_CHICK PRELIMINARY; PRT; 695 AA.
AC 09DGJ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NCLEOTIDE SEQUENCE.
RA Sarasa M., Rodolose A., Sorribas V.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -; mRNA.
DR HSP; Q16019; IYT.
DR SMK; Q9DGJ8; 28-123, 124-189, 385-494.
DR Ensembl; ENSGALG0000015770; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 3,1e-15;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 30

Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 626

RESULT 17

056UK4_CANFA PRELIMINARY; PRT; 714 AA.
AC 056UK4;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Beta-amyloid protein 714.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY26581; AAX81910.1; -; mRNA.
SQ SEQUENCE 714 AA; 80826 MW; 50DD51PB9E90ECS CRC64;

Query Match 100.0%; Score 162; DB 2; Length 714;

Best Local Similarity 100.0%; Pred. No. 3,2e-15;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 30

Db 616 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 645

RESULT 18

056UK2_STECO PRELIMINARY; PRT; 749 AA.
ID 056UK2_STECO PRELIMINARY; PRT; 749 AA.
AC 056UK2;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Beta-amyloid protein 749.
OS Stenella coeruleoalba (Striped dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Stenella.
OX NCBI_TaxID=9737;
RN [1]
RP NCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY26583; AAX81912.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:dimer binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
SQ SEQUENCE 749 AA; 84542 MW; 42659887C2A95D6 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 749;

Best Local Similarity 100.0%; Pred. No. 3,4e-15;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 30

Db 651 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGA 680

RESULT 19

A4_SAISC STANDARD; PRT; 751 AA.
ID A4_SAISC

AC 095241; (Ref. 37, Created)
 DT 15-DEC-1998 (Ref. 37, Last sequence update)
 DT 13-SEP-2005 (Ref. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE sorting homology) [contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (beta-Ap42);
 DE beta-amyloid protein 40 (beta-Ap40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Saimiri sciureus (common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
 OC Cebinae; Saimiri.
 OC NCBI_TaxID=9521;
 RN [1]
 NCULEOTIDE SEQUENCE:
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;
 RA Levy E., Amornin A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
 RT amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha Arpase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or its potentiated through Cu(2+)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoform that contains the BPTI domain
 CC possesses protease inhibitor activity (By similarity).
 CC FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPPR1, APPBP1, IBI, XNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DDB1.
 CC In vitro, it binds MAPT via the WT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via a clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;

CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not Described;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at App-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC Serine residues are neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; S81024; AAD14347.1; -; mRNA.
 CC PDB; 1RW6; X-ray; A=346-551.
 CC SMR; Q95241; 28-123, 124-189, 287-342.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR008154; A4_extra.
 CC InterPro; IPR001255; Beta-APP.
 CC InterPro; IPR002223; ProtInh_Kunz-m.
 CC PANTHER; PTHR10083:SF6; Beta-APP; 5.
 CC Pfam; PF02177; A4_EXTRA; 1.
 CC Pfam; PF03494; Beta-APP; 1.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOID4.
 CC PRINTS; PR00759; BASICPTASE.
 CC PRINTS; PR00204; BETAMYLOID.
 CC ProDom; PD000222; ProtInh_Kunz-m; 1.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.

KM 3D-structure; Alternative splicing; Amyloid; Apoptosis; Cell adhesion;
KM Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
KM Metal-binding; Notch signaling pathway; Phosphorylation;
KM Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
KM Transmembrane; Zinc.
FT SIGNAL 1 17 By similarity.
FT CHAIN 18 751 Amyloid beta A4 protein.
FT CHAIN 18 668 Soluble APP-alpha (Potential).
FT CHAIN 18 652 Soluble APP-beta (Potential).
FT CHAIN 653 751 C99 (Potential).
FT CHAIN 653 694 Beta-amyloid protein 42 (Potential).
FT CHAIN 653 692 Beta-amyloid protein 40 (Potential).
FT CHAIN 669 751 C83 (Potential).
FT PEPTIDE 669 694 P3(42) (Potential).
FT CHAIN 693 751 Gamma-CTF(59) (Potential).
FT CHAIN 695 751 Gamma-CTF(57) (Potential).
FT CHAIN 702 751 Gamma-CTF(50) (Potential).
FT CHAIN 721 751 C31 (Potential).
FT TOPO_DOM 18 680 Extracellular (Potential).
FT TRANSMEM 681 704 Potential.
FT TOPO_DOM 705 751 Cytoplasmic (Potential).
FT DOMAIN 291 341 BPT1/Kunitz inhibitor.
FT REGION 96 110 Heparin-binding (By similarity).
FT REGION 181 188 Zinc-binding (By similarity).
FT REGION 316 344 Heparin-binding (By similarity).
FT REGION 363 428 Heparin-binding (By similarity).
FT REGION 504 521 Collagen-binding (By similarity).
FT REGION 713 732 Interaction with G(o)-alpha (By similarity).
FT MOTIF 705 715 Basolateral sorting signal (By similarity).
FT MOTIF 740 743 NPXY motif.
FT COMPBIAS 230 260 Asp/Glu-rich (acidic).
FT COMPBIAS 274 280 Poly-Thr.
FT METAL 137 137 Copper (By similarity).
FT METAL 147 147 Copper (By similarity).
FT METAL 149 149 Copper (By similarity).
FT METAL 151 151 Copper (By similarity).
FT METAL 658 658 Copper or zinc (By similarity).
FT METAL 662 662 Copper or zinc (By similarity).
FT METAL 665 665 Copper or zinc (By similarity).
FT METAL 666 666 Copper or zinc (By similarity).
FT SITE 144 144 Required for Cu(2+) reduction (By similarity).
FT SITE 301 302 Reactive bond.
FT SITE 652 653 Cleavage (by beta-secretase) (By similarity).
FT SITE 653 654 Cleavage (by caspase-6) (By similarity).
FT SITE 668 669 Cleavage (by alpha-secretase) (By similarity).
FT SITE 685 685 Implicated in free radical propagation (By similarity).
Query Match 100.0%; Score 162; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGK 30
Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGK 682

RESULT 20
Q6GSC0 HUMAN PRELIMINARY; PRT; 751 AA.
AC Q6GSC0;
DT 05-JUL-2004 (Tremblere, 27, Created)
DT 05-JUL-2004 (Tremblere, 27, Last sequence update)
DT 05-JUL-2004 (Tremblere, 27, Last annotation update)
DE Amyloid beta A4 protein,, isoform b.
GN Name=APP;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uudin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.V., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
DR EMBL; BC065529; AAB65529.1; -; mRNA.
DR SRR; Q6GSC0; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSG00000142192; Homo sapiens.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0020037; F: heme binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:006118; P: electron transport; IEA.
DR InterPro; IPR008154; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR012282; Cytochrome_C_R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPT1; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE; PS02279; BPT1_KUNITZ_2; 1.
DR PROSITE; PS02279; BPT1_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84819 MW; C987C557C5A3714E CRC64;
Query Match 100.0%; Score 162; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGK 30
Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGK 682

RESULT 21
Q6RH28 CANFA PRELIMINARY; PRT; 751 AA.
ID Q6RH28 CANFA


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AC OGRH28;
DR 05-JUL-2004 (TReMBLrel. 27, Created)
DR 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DR 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP751.
GN Name=beta App;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RA Nakata M.; (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY498708; AAR97728.1; -; mRNA.
DR HSSP; Q16019; 1AAP.
DR SMR; OGRH28; 28-123, 124-189, 287-342, 441-550.
DR Ensemble1; ENSCAG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008154; A4_APP.
DR InterPro; IPR001255; A4_extra.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASB.
DR PRINTS; PR00204; BETAMAMLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84532 MW; 7541a947b46da54 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DAEFRHDSGYEVHOKLVFFPAEDVGSNKGA 30
DB 653 DAEFRHDSGYEVHOKLVFFPAEDVGSNKGA 682

RESULT 22
ID O56UK5_CANPA PRELIMINARY; PRT; 751 AA.
AC O56UK5;
DR 10-MAY-2005 (TReMBLrel. 30, Created)
DR 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DR 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Beta-amyloid protein 751.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RA Gallego C.; Sanchez-Diaz R.; Sarasa L.; Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926580; AAX81909.1; -; mRNA.
DR SMR; O56UK5; 28-123, 124-189, 287-342, 441-550.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
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DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_APP.
DR InterPro; IPR001255; A4_extra.
DR InterPro; IPR001285; Beta-APP.
DR InterPro; IPR012282; Cytochrome_C_R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASB.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84920 MW; C1CD20377DFF8550 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DAEFRHDSGYEVHOKLVFFPAEDVGSNKGA 30
DB 653 DAEFRHDSGYEVHOKLVFFPAEDVGSNKGA 682

RESULT 23
ID Q4R4R8_MACPA PRELIMINARY; PRT; 751 AA.
AC Q4R4R8;
DR 13-SEP-2005 (TReMBLrel. 31, Created)
DR 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DR 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Brain cDNA, clone: OFJA-13524, similar to human amyloid beta (A4)
DE protein (protease nexin-II, Alzheimer disease) (APP), transcript
DE variant 2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NOCLEOTIDE SEQUENCE.
RA Oada N.; Hirata M.; Tanuma R.; Kusuda J.; Hida M.; Suzuki Y.;
RA Sugano S.; Gojobori T.; Shen J.C.-K.; Wu C.I.; Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AB169826; BA801907.1; -; mRNA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_C_R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASB.
DR PRINTS; PR00204; BETAMAMLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
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DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROTEASE.
SQ SEQUENCE 751 AA; 84817 MW; 83CD196AD355158 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3,4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEPFHDSGYEVHHOKLVFPADVGSNKGK 30
   |||||
Db 653 DAEPFHDSGYEVHHOKLVFPADVGSNKGK 682

RESULT 24
09DGJ7 CHICK
ID 09DGJ7_CHICK PRELIMINARY; PRT; 751 AA.
AC 09DGJ7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-amyloid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sarasa M., Rodolase A., Sorribas V.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF289219; AAC00594.1; -; mRNA.
DR HSSP; Q16019; 11YT.
DR SMK; 09DGJ7; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSGALG00000015770; Gallus gallus.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001355; Beta_APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMAMLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84705 MW; E7BE9413A8033D84 CRC64;

Query Match 100.0%; Score 162; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3,4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC Q60495; Q60495;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
DE soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE P3(40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN Name=APP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Liver;
RX MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
RN [2]
RP INTERACTION OF BETA-APP40 WITH APOE.
RX MEDLINE=98007700; PubMed=9349544;
RA Martel C.U., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT cerebral capillary sequestration and blood-brain barrier transport of
RT circulating Alzheimer's amyloid beta.";
RL J. Neurochem. 69:1995-2004(1997).
RN [3]
RP PROCESSING.
RX MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;
RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA Bigl V.;
RT "Guinea-pig primary cell cultures provide a model to study expression
RT and amyloidogenic processing of endogenous amyloid precursor
RT protein.";
RL Neuroscience 95:243-254(2000).
RN [4]
RP GAMMA-SECRETASE PROCESSING.
RX MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;
RA Pimpli T., Musunuru U., Yun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RT "A novel gamma-secretase assay based on detection of the putative C-
RT terminal fragment-gamma of amyloid beta protein precursor.";
RL J. Biol. Chem. 276:481-487(2001).
RN [5]
RP FUNCTION: Functions as a cell surface receptor and performs
RP physiological functions on the surface of neurons relevant to
RP neurite growth, neuronal adhesion and axonogenesis. Involved in
RP cell mobility and transcription regulation through protein-protein
RP interactions (By similarity). Can promote transcription activation
RP through binding to APBB1/Tipe6 and inhibit Notch signaling through
RP interaction with Numb (By similarity). Complex to apoptosis-
RP inducing pathways such as those mediated by G1O and JIP (By
RP similarity). Inhibits G1O alpha ATPase activity (By similarity).
RP Acts as a kinesin I membrane receptor, mediating the axonal
RP transport of beta-secretase and presenilin 1 (By similarity). May
RP be involved in copper homeostasis/oxidative stress through copper
RP ion reduction (By similarity). In vitro, copper-metalated APP
RP induces neuronal death directly or is potentiated through Cu(2+)-
RP regulated low-density lipoprotein oxidation (By similarity). Can
RP regulate neurite outgrowth through binding to components of the
RP extracellular matrix such as heparin and collagen I and IV (By
RP similarity). The splice isoforms that contain the BPTI domain
RP possess protease inhibitor activity (By similarity).
RN [6]
RP FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
RP with metal-reducing activity. Bind transient metals such as
RP copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
RP and apolipoproteins E and J in the CSF and to HDL particles in

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CC Plasma: Inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Apolipoproteins elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CIT peptides as well as the caspase-cleaved
 CC peptides, including C1, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APPs family members, the APOA
 CC family, MAPK1p1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPE, FFR1, APPP1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via Bass) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of ATP and in a
 CC kinesin-dependent manner (By similarity). Soluble A-beta40 binds
 CC all three isoforms of APOB, in vitro and in vivo. When lipidated,
 CC APOB3 appears to be the preferred amyloid binding isoform, while
 CC the APOB4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC apicgans;
 CC Name=APP770;
 CC IsoId=060495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=060495-2; Sequence=VSP_007221, VSP_007222;
 CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -1- INDUCTION: Increased levels during neuronal differentiation.
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -1- DOMAIN: The NPYX sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPYX motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPYX site is also involved in
 CC clathrin-mediated endocytosis.
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/icastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (A-beta40)
 CC and amyloid-beta 42 (A-beta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).
 CC -1- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).
 CC -1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,

CC the apicgans (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interact with other proteins.
 CC -1- PTM: Extracellular binding and interaction with copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X97631; CAA66230.1; -; mRNA.
 CC EMBL; X99198; CAA67589.1; -; mRNA.
 CC HSPSP; P08592; INMJ.
 CC DR SNR; Q60495; 28-123, 124-189, 287-342, 460-569.
 CC DR InterPro; IPR008155; A4 APP.
 CC DR InterPro; IPR008154; A4 extra.
 CC DR InterPro; IPR001255; Beta-APP.
 CC DR InterPro; IPR002223; Prot inh Kunz-m.
 CC DR PANTHER; PTHR10083:SF6; Beta-APP; 6.
 CC DR Pfam; PF02177; A4 EXTRA; 1.
 CC DR Pfam; PF03494; Beta-APP; 1.
 CC DR Pfam; PF00014; Kunitz BPTI; 1.
 CC DR PRINTS; PR00203; AMYLOIDA4.
 CC DR PRINTS; PR00759; BASICPTASB.
 CC DR PRINTS; PR00204; BETAMVLOID.
 CC DR ProDom; PD000222; Prot inh Kunz-m; 1.
 CC DR SMART; SM00006; A4 EXTRA; 1.
 CC DR SMART; SM00131; KU7; 1.
 CC DR PROSITE; PS00319; A4 EXTRA; 1.
 CC DR PROSITE; PS00320; A4 INTRA; 1.
 CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 CC KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
 CC Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
 CC Metal-binding; Notch signaling pathway; Phosphorylation;
 CC KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 CC Tmembrane; Zinc.
 CC FT SIGNAL 1 17 By similarity.
 CC FT CHAIN 18 770 Amyloid beta A4 protein.
 CC FT CHAIN 18 687 Soluble APP-alpha (By similarity).
 CC FT CHAIN 18 671 Soluble APP-beta (By similarity).
 CC FT CHAIN 672 770 CTF-alpha (By similarity).
 CC FT CHAIN 672 713 Beta-amyloid protein 42 (By similarity).
 CC
 CC Query Match 100.0%; Score 162; DB 1; Length 770;
 CC Best Local Similarity 100.0%; Pred. No. 3, 5e-15;
 CC Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGK 30
 CC Db 672 DAEFRHDSGYEVHOKLVFPAEDVGSNKGK 701
 CC
 CC RESULT 26
 CC ID A4 HUMAN STANDARD; PRT; 770 AA.
 CC AC P05067; P09000; P78438; Q13764; Q13793; Q16011; Q16014;
 CC AC Q16019; Q16020; Q9RT38; Q9UC29; Q9UCB6; Q9UCB8; Q9UCD1; Q9UC05;
 CC DT 13-AUG-1987 (Rel. 05, Created)
 CC DT 01-NOV-1991 (Rel. 20, Last sequence update)
 CC DT 13-SEP-2005 (Rel. 48, Last annotation update)
 CC DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 CC amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease

DE nexin-II) (PN-II) (APP1) [Contains: Soluble APP-alpha (S-APP-
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (beta-APP42); Beta-amyloid protein 40 (beta-APP40); C83; P3(42);
 DE P3(40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59)
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CRF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CRF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN Name=APP; Synonyms=A4, AD1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 ON [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207; DOI=10.1038/325733a0;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Greschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor";
 RL Nature 325:733-736(1987).
 RL [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289; DOI=10.1038/331525a0;
 RA Ponte P., Gonzalez-Dewhite P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors";
 RL Nature 331:525-527(1988).
 RL [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is
 RT encoded by 16 exons";
 RL Nucleic Acids Res. 17:517-522(1989).
 RL [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=90233318; PubMed=2110105; DOI=10.1016/0378-1119(90)90310-N;
 RA Yoshitai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene";
 RL Gene 87:257-263(1990).
 RL [5]
 RP ERRATUM.
 RX PubMed=1908403; DOI=10.1016/0378-1119(91)90093-Q;
 RA Yoshitai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
 RL Gene 102:291-292(1991).
 RL [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Krenzelok G., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RL [7]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164; DOI=10.1093/nar/25.9.1802;
 RA Hattori M., Tsukihara F., Furuhara Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sasaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).

RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RX DOI=10.1046/j.1460-9568.2003.02731.x;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RL [9]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LYS-501.
 RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
 RA Nguyen C.P., Gilderleeve H., Cassidy C.M., Johnson E.J.,
 RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
 RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RL [10]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS APP305 AND APP751).
 RC TISSUE=Eye, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Abramson R.D., Mullaby S.J.,
 RA Raba S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton R., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rutherfordfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schenck A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [11]
 RP NUCLEOTIDE SEQUENCE OF 1-10.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RL [12]
 RP ERRATUM, AND SEQUENCE REVISION.
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RL [13]
 RP NUCLEOTIDE SEQUENCE OF 1-75.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakia N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RL [14]
 RP PROTEIN SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RL [15]
 RP PROTEIN SEQUENCE OF 18-40.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals W., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides";

RL Nat. Biotechnol. 21:566-569(2003).
RN [16]
RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.,
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RL secreted protein.";
RN Science 245:651-653(1989).
RN [17]
RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Winiowski H.M.,
RT "Molecular cloning and characterization of a cDNA encoding the
RL cerebrovascular and the neuritic plaque amyloid peptides.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [18]
RP NUCLEOTIDE SEQUENCE OF 286-366.
RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.,
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RL mRNA associated with Alzheimer's disease.";
RN Nature 331:528-530(1988).
RN [19]
RP NUCLEOTIDE SEQUENCE OF 287-367.
RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.,
RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
RL inhibitory activity.";
RN Nature 331:530-532(1988).
RN [20]
RP NUCLEOTIDE SEQUENCE OF 507-770.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zein S.B., Sallim M., Chou W.G., Sajdel-Sulowska E.M., Majocha R.E.,
RA Marotta C.A.,
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RL disease brain: coding and noncoding regions of the fetal precursor
RN mRNA are expressed in the cortex.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [21]
RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96135497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
RA Behner D., Heese L., Masters C.L., Multhaup G.,
Query Match 100.0%; Score 162; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3, 5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGK 30
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGK 701
RESULT 27
A4 MACFA STANDARD; PRT; 770 AA.
ID AC P53601; Q60HH7; Q95KN7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Amyloid beta A4 protein precursor (ABPP) (Alzheimer's disease
DE amyloid beta A4 protein precursor (ABPP) (Alzheimer's disease
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59) (Gamma-
DE secretase C-terminal fragment 57) (Gamma-CRF(57)
DE secretase C-terminal fragment 50) (C31).
GN Name=APP; ORFNames=OCCE-15949;
OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey).
OC Bkaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlasky M.B., Toland D.R., Selkoe D.J.,
RT Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RL disease.";
RN Am. J. Pathol. 138:1423-1435(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Brain cortex;
RA Kusuda J., Osada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.,
RT "Isolation and characterization of cDNA for macaque neurological
RL disease genes.";
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(2+)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -1- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -1- SUBUNIT: Binds, via its C-terminus, to the P1D domain of several
CC cytoplasmic proteins, including APBB family members, the APPA
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPT, FRHL1, APBB1, B1, KIN2
CC (via its TRP domains) (By similarity), APBB2 (via Bass) and DDB1.
CC In vitro, it binds MAPT with the microtubule-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via a clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CRF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Comment=Alternative splicing: Named isoforms=3;
CC Name=APP770;
CC Name=P53601-1; Sequence=Displayed;
CC Name=APP695;
CC Name=P53601-2; Sequence=VSP_000010, VSP_000011;
CC Name=3;
CC IsoId=P53601-3; Sequence=VSP_013360, VSP_013361;

CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides. S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/ncastatin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-2, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; M58726; AAA36828.1; -; mRNA.
 DR EMBL; M58727; AAA36829.1; -; mRNA.
 DR EMBL; AB125150; BAD51938.1; -; mRNA.
 DR HSSP; P08592; INMJ.
 DR SMK; P53601; 28-123, 124-189, 287-342, 460-569.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002233; Prot_inh_Kunz-m.
 DR PANTHER; PTHR10083; SF6; Beta-APP; 6.
 DR Pfam; Pf02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICTASB.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;

KW Metal-binding; Notch signaling pathway; Phosphorylation;
 KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 KW Transmembrane; Zinc.

FT	SIGNAL	1	17	
FT	CHAIN	18	770	By similarity.
FT	CHAIN	18	687	Amyloid beta A4 protein.
FT	CHAIN	18	671	Soluble APP-alpha (Potential).
FT	CHAIN	672	770	Soluble APP-beta (Potential).
FT	CHAIN	672	713	C99 (Potential).
FT	CHAIN	672	711	Beta-amyloid protein 42 (Potential).
FT	CHAIN	672	711	Beta-amyloid protein 40 (Potential).
FT	CHAIN	688	770	C83 (Potential).
FT	PEPTIDE	688	713	P3(42) (Potential).
FT	PEPTIDE	688	711	P3(40) (Potential).
FT	CHAIN	712	770	Gamma-CTF(59) (Potential).
FT	CHAIN	714	770	Gamma-CTF(57) (Potential).
FT	CHAIN	721	770	Gamma-CTF(50) (Potential).
FT	CHAIN	740	770	C31 (Potential).
FT	TOPO_DOM	18	699	Extracellular (Potential).
FT	TRANSMEM	700	723	Potential.
FT	TOPO_DOM	724	770	Cytoplasmic (Potential).
FT	DOMAIN	291	341	BPTI/Kunitz inhibitor.
FT	REGION	96	110	Heparin-binding (By similarity).
FT	REGION	181	188	Zinc-binding (By similarity).
FT	REGION	391	423	Heparin-binding (By similarity).
FT	REGION	491	522	Heparin-binding (By similarity).
FT	REGION	523	540	Collagen-binding (By similarity).
FT	REGION	732	751	Interaction with G(c)-alpha (By similarity).
FT	MOTIF	724	734	Basolateral sorting signal (By similarity).
FT	MOTIF	759	762	NPXY motif.
FT	COMPBAS	230	260	Asp/Glu-rich (acidic).
FT	COMPBAS	274	280	Poly-Thr.
FT	METAL	137	137	Copper (By similarity).
FT	METAL	147	147	Copper (By similarity).
FT	METAL	149	149	Copper (By similarity).
FT	METAL	151	151	Copper (By similarity).
FT	METAL	677	677	Copper or zinc (By similarity).
FT	METAL	681	681	Copper or zinc (By similarity).

Query Match 100.0%; Score 163; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGVEVHOKLVFAEDVGNKGA 30
 DB 672 DAERFHDGVEVHOKLVFAEDVGNKGA 701

RESULT 28
 A4_PANTH STANDARD; PRT; 770 AA.
 ID A4_PANTH
 AC Q5IS80;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name:APP;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP NCBIOTIDE SEQUENCE [MRNA].
 RX PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
 RA Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,

RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
RT "Accelerated evolution of nervous system genes in the origin of Homo
Cell 119:1027-1040(2004).
CC -1- FUNCTION: Functions as a cell surface receptor and performs
physiological functions on the surface of neurons relevant to
neural growth, neuronal adhesion and axonogenesis. Involved in
cell motility and transcription regulation through protein-protein
interactions (By similarity). Can promote transcription activation
through binding to APBB1/Tipe0 and inhibit Notch signaling through
interaction with Numb (By similarity). Couples to apoptosis-
inducing pathways such as those mediated by G(O) and JIP (By
similarity). Inhibits G(O) alpha ATPase activity (By similarity).
Acts as a kinesin I membrane receptor, mediating the axonal
transport of beta-secretase and presenilin 1 (By similarity). May
be involved in copper homeostasis/oxidative stress through copper
ion reduction. In vitro, copper-metalated APP induces neuronal
death directly or is potentiated through Cu(2+)-mediated low-
density lipoprotein oxidation (By similarity). Can regulate
neurite outgrowth through binding to components of the
extracellular matrix such as heparin and collagen I and IV (By
similarity). The splice isoforms that contain the BPTI domain
possess protease inhibitor activity (By similarity).
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
with metal-reducing activity. Bind transient metals such as
copper, zinc and iron (By similarity).
CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
apoptosis (By similarity).
CC -1- STRUTIT: Binds, via its C-terminus, to the PID domain of several
cytoplasmic proteins including APPA family members, the APPA
family MAPK3p1 and SHC1. Numb and Dab1 (By similarity). Binding
to Dab1 inhibits its serine phosphorylation (By similarity). Also
interacts with GPCR-like protein APP, PP2A, APPBP1, It1, KNS2
(via its TPR domains) (By similarity). APPBP2 (via Bass) and DDB1.
In vitro, it binds MAP2 via the MT-binding domains (By
similarity). Associates with microtubules in the presence of ATP
and in a kinesin-dependent manner (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
protein that rapidly becomes internalized via a clathrin-coated
pit. During maturation, the immature APP (N-glycosylated in the
endoplasmic reticulum) moves to the Golgi where complete
maturation occurs (O-glycosylated and sulfated). After alpha-
secretase cleavage, soluble APP is released into the extracellular
space and the C-terminal is internalized into the endosomes and
lysosomes. Some APP accumulates in secretory transport vesicles
leaving the late Golgi compartment and returns to the cell
surface. Gamma-CTF(59) peptide is located to both the cytoplasm
and nucleus of neurons (By similarity).
CC -1- DOMAIN: The basolateral sorting signal (Bass) is required for
sorting of membrane proteins to the basolateral surface of
epithelial cells (By similarity).
CC -1- DOMAIN: The NPYX sequence motif found in many tyrosine-
phosphorylated proteins is required for the specific binding of
the PID domain. However additional amino acids either N- or C-
terminal to the NPYX motif are often required for complete
interaction. The PID domain-containing proteins which bind APP
require the YENPTY motif for full interaction. These interactions
are independent of phosphorylation on the terminal tyrosine
residue. The NPYX site is also involved in clathrin-mediated
endocytosis (By similarity).
CC -1- PTM: Proteolytically processed under normal cellular conditions.
Cleavage by alpha-secretase or alternatively by beta-secretase
leads to generation and extracellular release of soluble APP
peptides, S-APP-alpha and S-APP-beta, respectively, and the
retention of corresponding membrane-anchored C-terminal fragments,
C83 and C99. Subsequent processing of C83 by gamma-secretase
yields p3 peptides. This is the major secretory pathway and is
nonamyloidogenic. Alternatively, presenilin/epsilon-mediated
gamma-secretase processing of C99 preserves the amyloid beta
proteins, amyloid-beta 40 (beta40) and amyloid-beta 42 (beta42).
Major components of amyloid plaques, and the cytotoxic C-terminal
fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By

similarity).
CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
(By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
results in the production of the neurotoxic C31 peptide and the
increased production of beta-amyloid peptides (By similarity).
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
serine residues is neuron-specific. Phosphorylation can affect APP
processing, neuronal differentiation and interaction with other
proteins (By similarity).
CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
zinc, can induce histidine-bridging between beta-amyloid molecules
resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
inhibits collagen-binding (By similarity).
CC -1- SIMILARITY: Belongs to the APP family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL: A565248; AAV74286.1; -; mRNA.
CC SMR: Q51S80; 28-123, 124-189, 287-342, 460-569.
CC InterPro: IPR008155; A4-APP.
CC InterPro: IPR008154; A4-extra.
CC InterPro: IPR001255; Beta-APP.
CC InterPro: IPR012282; Cytochrome c R.
CC InterPro: IPR002223; Prot_inh_Kunz-m.
CC PANTHER: PTHR10083:SF6; Beta-APP; 6.
CC Pfam: PF02177; A4-EXTRA; 1.
CC Pfam: PF00344; Beta-APP; 1.
CC Pfam: PF00014; Kunitz-BPTI; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC PRINTS: PR00759; BASICPTSR.
CC PRINTS: PR00264; BPTAMYLOID.
CC PRODOM: PD00022; Prot_inh_Kunz-m; 1.
CC SMART: SM00006; A4-EXTRA; 1.
CC SMART: SM00319; KUF_1.
CC PROSITE: PS00320; BPTI_KUNITZ_1.
CC PROSITE: PS00280; BPTI_KUNITZ_2.
CC PROSITE: PS00279; BPTI_KUNITZ_1.
CC PROSITE: PS00279; BPTI_KUNITZ_2.
CC Amyloid, Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
KW Notch signaling pathway; Heparin-binding; Iron; Metal-binding;
KW Glycoprotein; Heparin-binding; Iron; Metal-binding;
KW Notch signaling pathway; Phosphorylation; Protease inhibitor; Zinc.
KW Proteoglycan; Serine protease
FT SIGNAL 1 17
FT CHAIN 18 770
FT CHAIN 18 687
FT CHAIN 18 671
FT CHAIN 672 770
FT CHAIN 672 713
FT CHAIN 672 711
FT CHAIN 688 770
FT CHAIN 688 713
FT PEPTIDE 688 711
FT CHAIN 712 770
FT CHAIN 714 770
FT CHAIN 721 770
FT CHAIN 740 770
FT CHAIN 18 699
FT TOPO_DOM 700 723
FT TRANSMEM 724 770
FT TOPO_DOM 724 770
FT DOMAIN 291 341
FT REGION 96 110
FT REGION 181 188
FT REGION 391 423
FT REGION 491 522
FT REGION 523 540
FT REGION 732 751
Interaction with G(O)-alpha (By

FT	MOTIF	724	734	similarity).
FT	MOTIF	759	762	Basolateral sorting signal (By
FT	COMPBIAS	230	260	similarity).
FT	COMPBIAS	274	280	NPXY motif.
FT	METAL	137	137	Asp/Gln-rich (acidic).
FT	METAL	147	147	Poly-Thr.
FT	METAL	149	149	Copper (By similarity).
FT	METAL	151	151	Copper (By similarity).
FT	METAL	677	677	Copper (By similarity).
FT	METAL	681	681	Copper or zinc (By similarity).
FT	METAL	684	684	Copper or zinc (By similarity).
FT	METAL	685	685	Copper or zinc (By similarity).
FT	METAL	144	144	Required for Cu(2+) reduction (By
FT	SITE	301	302	similarity).
FT	SITE	671	672	Reactive bond (By similarity).
FT	SITE	672	673	Cleavage (by beta-secretase) (By
FT	SITE	687	688	similarity).
FT	SITE	704	704	Cleavage (by caspase-6) (By similarity).
FT	SITE	706	706	Cleavage (by alpha-secretase) (By
FT	SITE	711	712	similarity).
FT	SITE	713	714	Implicated in free radical propagation
FT	SITE	720	721	(By similarity).
FT	SITE	739	740	Susceptible to oxidation (By similarity).
FT	SITE			Cleavage (by gamma-secretase; site 1) (By
FT	SITE			similarity).
FT	SITE			Cleavage (by gamma-secretase; site 2) (By
FT	SITE			similarity).
FT	SITE			Cleavage (by gamma-secretase; site 3) (By
FT	SITE			similarity).
FT	SITE			Cleavage (by caspases-6, -8 or -9) (By
FT	SITE			similarity).

Query Match 100.0%; Score 162; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 3; Se-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPFHDSGYVHHOKLVFPFEDVSNKGA 30
 DB 672 DAEPFHDSGYVHHOKLVFPFEDVSNKGA 701

RESULT 29

A4_PIG STANDARD; PRT; 770 AA.
 AC P79307; Q29023; Q9TUI0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C311).
 GN Name=APP;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kimura A., Takahashi T.;
 RC "Amyloid precursor protein 770."
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-136.
 RA Wittwe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library."

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN NUCLEOTIDE SEQUENCE OF 667-723.
 RP TISSUE=Brain;
 RC MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK3ip1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APBBP1, J31, KNS2
 CC (via its TTR domains) (By similarity), APPBP2 (via Bass) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields p3 peptides. This is the major secretory pathway and is

CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).
CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -1- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity). APP and
CC extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -1- SIMILARITY: Belongs to the APP family.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AB032550; BAA84580.1; -, mRNA.
CC EMBL: Z84022; CAB06313.1; -, mRNA.
CC EMBL: X56127; CAJ39592.1; -, mRNA.
CC HSSP: P08592; 1NMJ.
CC DR SNR; P79307; 28-123, 124-189, 287-342, 460-569.
CC DR Interpro: IPR008155; A4_APP.
CC DR Interpro: IPR008154; A4_extra.
CC DR Interpro: IPR001255; Beta-APP.
CC DR Interpro: IPR002223; Prot_inh_Kunz-m.
CC DR PANTHER: PTHR10083.Sf6; Beta-APP; 6.
CC DR Pfam: PF02177; A4_EXTRA; 1.
CC DR Pfam: PF03494; Beta-APP; 1.
CC DR Pfam: PF00014; Kunitz_BPTI; 1.
CC DR PRINTS: PR00203; AMYLOIDA4.
CC DR PRINTS: PR00759; BASICPTASE.
CC DR PRINTS: PR00204; BETAMYOLOID.
CC DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
CC DR SMART: SM00006; A4_EXTRA; 1.
CC DR SMART: SM00331; KU; 1.
CC DR PROSITE: PS00319; A4_EXTRA; 1.
CC DR PROSITE: PS00320; A4_INTRA; 1.
CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
CC DR Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
CC Notch signaling pathway; Phosphorylation; Protease inhibitor;
CC KM Serine protease inhibitor; Signal; Transmembrane; Zinc.
CC FT SIGNAL 1 17
FT CHAIN 18 770 Amyloid beta A4 protein.
FT CHAIN 18 687 Soluble APP-alpha (Potential).
FT CHAIN 18 671 Soluble APP-beta (Potential).
FT CHAIN 672 770 C99 (By similarity).
FT CHAIN 672 713 Beta-amyloid protein 40 (By similarity).
FT CHAIN 672 711 Beta-amyloid protein 42 (By similarity).
FT CHAIN 688 770 C83 (By similarity).
FT CHAIN 688 713 P3(42) (By similarity).
FT CHAIN 688 711 P3(40) (By similarity).
FT PEPTIDE 712 770 Gamma-CTF(59).
FT CHAIN 714 770 Gamma-CTF(50).
FT CHAIN 721 770 Gamma-CTF(50) (By similarity).
FT CHAIN 740 770 C31 (By similarity).
FT CHAIN

FT TOPO DOM 18 699 Extracellular (Potential).
FT TRANSMEM 723 723 Potential.
FT TOPO DOM 724 770 Cytoplasmic (Potential).
FT DOMAIN 291 341 BPTI/Kunitz inhibitor.
FT REGION 96 110 Heparin-binding (By similarity).
FT REGION 135 155 Copper-binding (By similarity).
FT REGION 181 188 Zinc-binding (By similarity).
FT REGION 391 423 Heparin-binding (By similarity).
FT REGION 491 522 Heparin-binding (By similarity).
FT REGION 523 540 Collagen-binding (By similarity).
FT REGION 732 751 Interaction with G(c)-alpha (By similarity).
FT MOTIF 724 734 Basolateral sorting signal.
FT MOTIF 759 762 NPXY motif.
FT COMPBIAS 230 260 Asp/Glu-rich (acidic).
FT COMPBIAS 274 280 Poly-Thr.
FT METAL 137 137 Copper (By similarity).
FT METAL 147 147 Copper (By similarity).
FT METAL 149 149 Copper (By similarity).
FT METAL 151 151 Copper (Probable).
FT METAL 671 677 Copper or zinc (By similarity).
FT METAL 681 684 Copper or zinc (By similarity).
FT METAL 684 684 Copper or zinc (By similarity).
FT METAL 685 685 Copper or zinc (By similarity).
FT SITE 144 144 Required for Cu(2+) reduction (By similarity).

Query Match 100.0%; Score 162; DB 1; Length 770;
Best Local Similarity 100.0%; Pred No. 3; Se-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPFUDSGYVHOKLVFPAEDVGNKCA 30
DB 672 DAEPFUDSGYVHOKLVFPAEDVGNKCA 701
|||||

RESULT 30
ID Q6RH30_CANPA PRELIMINARY; PRT; 770 AA.
AC Q6RH30;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP770.
GN Name=Beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1] TaxID=9615;
RX NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RP Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AY498706; AAR97726.1; -, mRNA.
DR HSSP: Q16019; 1AAP.
DR SNR; Q6RH30; 28-123, 124-189, 287-342, 460-569.
DR Ensemble; ENSCAG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Interpro: IPR008155; A4_APP.
DR Interpro: IPR001255; Beta-APP.
DR Interpro: IPR001255; A4_extra.
DR Interpro: IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMYOLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.

[illegible]

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kaakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cabaavnt T.,
RA Fleischmann W., Gaasterland T., Glasl C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guestinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohntski S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.",
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Yoneda S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanaki M.,
RA Furekawa Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kanakawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numasaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK076506; BAC36369.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR SMR; O8BPC7; 74-183.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C:integral to membrane, IDA.
DR GO; GO:0016020; C:membrane, TAS.
DR GO; GO:0005515; F:protein binding, IPI.

DR GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER
SQ SEQUENCE 364 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 88.3%; Score 143; DB 2; Length 384;
Best Local Similarity 90.0%; Pred. No. 1,le-12;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYVHHQKLVFFAEDVGSNKG 30
DB 286 DAFFRHDSGYVHHQKLVFFAEDVGSNKG 315

RESULT 36

O98SGO_XENLA

ID O98SGO_XENLA PRELIMINARY; PRT; 693 AA.

AC O98SGO; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Beta-amyloid precursor protein A.

GN Name=app;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;

OC Xenopodinae; Xenopus; Xenopus.

CX NCBI_Taxid=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=21610087; PubMed=11744158; DOI=10.1016/S0169-328X(01)00279-0;

RA Van den Hark W.H., Bloemen M., Martens G.J.M.,

RT "Expression of the gene encoding the beta-amyloid precursor protein
RT App in Xenopus laevis.",
RL Brain Res. Mol. Brain Res. 97:13-20(2001).
RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Van den Hark W.H.,

RL Thesis (2001), Department of Biological Sciences, University of
NL Nijmegen, Nijmegen, Netherlands.
RX EMBL; AJ298150; CAC37193.1; -; mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; O98SGO; 27-122, 383-492.
DR GO; GO:0016021; C:integral to membrane, IEA.
DR GO; GO:0005488; P:binding, IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4 EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78567 MW; CAFIDP655CLAB653 CRC64;

Query Match 88.3%; Score 143; DB 2; Length 693;
Best Local Similarity 83.3%; Pred. No. 2,2e-12;
Matches 25; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYVHHQKLVFFAEDVGSNKG 30
DB 595 DSEYRHDTAYEVHHQKLVFFAEDVGSNKG 624


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OX NCBI_TaxID=8353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93129227; PubMed=1282805;
RA Okado H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression."
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: S52417; AAB24853.1; -; mRNA.
DR HSSP: Q16019; 1H23.
DR SMK: Q91963; 26-119, 283-338, 437-546.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMAMLOID.
DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75E81865681D948 CRC64;

Query Match 88.3%; Score 143; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 2,4e-12;
Matches 25; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKG 30
DB 649 DSEYRHDYAVEVHHQKLVFPADVGSNKG 678

RESULT 40
OGNR1_XENLA PRELIMINARY; PRT; 749 AA.
ID OGNR1_XENLA PRELIMINARY;
AC OGNR1_XENLA PRELIMINARY;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE App protein.
GN Name=app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: BC070668; AAB70668.1; -; mRNA.
DR HSSP: Q16019; 1BA4.
DR SMK: OGNR1; 27-122, 285-340, 439-548.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

Query Match 88.3%; Score 143; DB 2; Length 749;
Best Local Similarity 83.3%; Pred. No. 2,4e-12;
Matches 25; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKG 30
DB 651 DSEYRHDYAVEVHHQKLVFPADVGSNKG 680

RESULT 41
OGDJB6_XENR PRELIMINARY; PRT; 750 AA.
ID OGDJB6_XENR PRELIMINARY;
AC OGDJB6_XENR PRELIMINARY;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Amyloid beta (A4) protein (Protease nexin-II, Alzheimer disease).
GN Name=app;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Whole body;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hutcheson S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Whole body;
 RC Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL: BC075266; AAF75266.1; -; mRNA.
 DR SMR: O6DJB6: 27-122, 285-340, 440-549.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR006155; A4_APP.
 DR InterPro: IPR008154; A4_APP.
 DR InterPro: IPR001253; Beta-APP.
 DR InterPro: IPR002223; Prot_inh_Kunz-m.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR PRINTS: PR00759; BAKICITASE.
 DR PRINTS: PR00204; BETAAMYLOID.
 DR PRINTS: PR000222; Prot_inh_Kunz-m; 1.
 DR SMART: SM00131; KU; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_EXTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Peptidase.
 SQ SSOURCE: 750 AA; 84927 MW; 4222350843147CAF CRC64;
 Query Match 88.3%; Score 143; DB 2; Length 750;
 Best Local Similarity 83.3%; Pred. No. 2,4e-12;
 Matches 25; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DAERHDSGYEVHOKLVFAEDVGSNKA 30
 DB 652 DSEYRDAAVEVHOKLVFAEVEGSKGA 681
 A4_MOUSE STANDARD; PRT; 770 AA.
 AC P13023; P97487; P97942; O99K32;
 DT 01-OCT-1989 (Ref. 12, Created);
 DT 10-OCT-2003 (Ref. 42, Last sequence update);
 DT 13-SEP-2005 (Ref. 48, Last annotation update);
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease
 DE amyloid protein homologue) (amyloidogenic glycoprotein) (AG) [contains:
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein

DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
 DE (APP-C99); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
 DE (Amyloid intracellular domain 57) (AID(57)) (APP-C97); Gamma-CTF(50)
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
 DE 50) (AID(50)); C31].
 GN Name=APP;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RP TISSUE=Brain;
 RC MEDLINE=88106489; PubMed=3322280;
 RX Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.,
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671 (1987).
 [2]
 RN SEQUENCE REVISION.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 [3]
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RP STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177; DOI=10.1016/0167-4781(91)90231-A;
 RA de Strooper B., Van Leuven F., Van den Berghe H.,
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closely related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143 (1991).
 [4]
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RP STRAIN=SAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921; DOI=10.1139/bcb-79-1-57;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhireju C.,
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67 (2001).
 [5]
 RN NUCLEOTIDE SEQUENCE OF 1-19.
 RX MEDLINE=92209398; PubMed=1555768; DOI=10.1016/0378-1119(92)90375-Y;
 RA Izumi R., Yamada T., Toshiaki S.I., Sasaki H., Hatori M., Sakai Y.,
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 118:189-195 (1992).
 [6]
 RN PARTIAL NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM APP770).
 RP TISSUE=Mammary tumor;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hutcheson S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [7]

RP NUCLEOTIDE SEQUENCE OF 281-380, AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 289-364.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domestica";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP NUCLEOTIDE SEQUENCE OF 656-737.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Saffield F., Duff K., Korenblatt K., Capecci M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93387808; PubMed=8510506; DOI=10.1016/0169-328X(93)90020-P;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triahou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and homozygous
 RT weaver mutant mice as revealed by in situ hybridization
 RT histochemistry";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=1144355; DOI=10.1016/S0896-6273(00)00124-0;
 RA Kamal A., Stockin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-I";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Macuda S., Yasukawa T., Homma Y., Ito Y., Nikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/Islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=220208091; PubMed=11912189; DOI=10.1074/jbc.M108372200;
 RA Tani H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN [14]
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.
 RX MEDLINE=22008109; PubMed=12011466; DOI=10.1073/pnas.102192599;
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.R., Lopez P.A.,
 RA Meucci O., McLade J.C., Rakic P., D'Adamo L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid
 RT precursor protein binds Numb and inhibits Notch signaling";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APPB1.
 RX MEDLINE=21437805; PubMed=11553691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a

RT nuclear fraction of neurons in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APPB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPTI domain possess protease inhibitor activity (By
 CC similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transition metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transition metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPX II-
 CC mediated phosphorylation (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APPA
 CC family, MAPKIP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPP, FPR1, APPB1, IBI, KNS2 (via its TPR domain), APPB2 (via
 CC BABS) and DDB1 (By similarity). In vitro, it binds MAPT via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of ATP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HMDH2 (By
 CC similarity).
 CC -1- INTERACTION:
 CC P98084: Appa2; NDEXP=1; INFACT=EBI-78814; EBI-81669;
 CC Q9GXU1: Appb1; NDEXP=1; INFACT=EBI-78814; EBI-81338;
 CC P97318: Dab1; NDEXP=1; INFACT=EBI-78814; EBI-81680;
 CC
 CC Query Match 88.3%; Score 143; DB 1; Length 770;
 CC Best Local Similarity 90.0%; Pred. No. 2,4e-12;
 CC Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 1 DAEPHDSGVVHHOKLVFPAEDVGSNKG 30
 CC DB 672 DAEPHDSGVFVRHOKLVFPAEDVGSNKG 701
 CC
 CC
 CC RESULT 43
 CC A4_RAT STANDARD; PRT; 770 AA.
 CC ID A4_RAT P08592;
 CC AC 01-AUG-1988 (Rel. 08, Created)
 CC DT 01-DEC-1992 (Rel. 24, Last sequence update)
 CC DT 13-SEP-2005 (Rel. 48, Last annotation update)
 CC DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 CC protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
 CC APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
 CC amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
 CC C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
 CC fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
 CC DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
 CC GN Name=APP;
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2300758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RN Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in
RT rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP PROTEIN SEQUENCE OF 18-44.
RX MEDLINE=88264430; PubMed=2368652;
RA Schubert D., Schroeder R., Lacorbiere M., Saitoh T., Cole G.;
RT "Amyloid beta protein precursor is possibly a heparan sulfate
RT proteoglycan core protein.";
RL Science 241:223-226(1988).
RN [3]
RP PROTEIN SEQUENCE OF 18-32.
RX MEDLINE=91217087; PubMed=1673681;
RA Potempa A., Styles J., Mehta P., Kim K.S., Miller D.L.;
RT "Purification and tissue level of the beta-amyloid peptide precursor
RT of rat brain.";
RL J. Biol. Chem. 266:8464-8469(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 289-364.
RC TISSUE=Liver;
RX MEDLINE=889181525; PubMed=2648331;
RA King U., Mueller-Hill B.;
RT "The sequence of the two 5' extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2139(1989).
RN [5]
RP PROTEIN SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX MEDLINE=21443797; PubMed=1183588; DOI=10.1074/jbc.C100357200;
RA Gu Y., Miesnow H., Sato T., Dohme N., Tekio K., Inara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [6]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96187032; PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [7]
RP TISSUE SPECIFICITY OF APPICAN.
RX MEDLINE=95563526; PubMed=7744833; DOI=10.1074/jbc.270.20.11839;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliadou D.,
RN Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [8]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=97150061; PubMed=8996834;
RA Sandbrink R., Montag U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [9]
RP INTERACTION WITH DBP1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX MEDLINE=99127916; PubMed=930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RN Suzuki K., Naito A.C., Stengard P.;
RT "A 127-kDa protein (UV-DB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [10]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.

RX MEDLINE=99162676; PubMed=10024358;
RA Brouillet E., Tremblay A., Galiana D., Volovitch M., Bouillat C.,
RN Valenza C., Prochiantz A., Alliquand B.;
RT "The amyloid precursor protein interacts with G heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [11]
RP COPPER-BINDING.
RX MEDLINE=94320627; PubMed=7913895; DOI=10.1016/0014-5793(94)00658-X;
RA Heese L., Behner D., Masters C.L., Multhaup G.;
RT "The beta A4 amyloid precursor protein binding to copper.";
RL FEBS Lett. 349:109-116(1994).
RN [12]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970; DOI=10.1074/jbc.270.18.10388;
RA Pangalos M.N., Efthymiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [13]
RP BETA-AMYLOID METAL-BINDING.
RX MEDLINE=99316162; PubMed=1036699; DOI=10.1021/bj990438f;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RN Scarpa R.C., Cuaungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RT "Type A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [14]
RP BETA-AMYLOID ZINC-BINDING.
RX MEDLINE=99343552; PubMed=10413512; DOI=10.1021/bj9902050;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [15]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX MEDLINE=21956095; PubMed=11959460; DOI=10.1016/S0925-4439(01)00097-7;
RA Kaneki J., Varadarajan S., Akenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochim. Biophys. Acta 1586:190-198(2001).
RN [16]
RP PHOSPHORYLATION.
RX MEDLINE=97239592; PubMed=9085254;
RA Oehl M., Naito A.C., Czernik A.O., Lim G.S., Isohara T., Gandy S.E.,
RN Greengard P., Suzuki T.;
RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT cultured cells.";
RL Mol. Med. 3:111-123(1997).
RN [17]
RP PHOSPHORYLATION SITE SER-730.
RX MEDLINE=99262094; PubMed=10329382; DOI=10.1006/brc.1999.0637;
RA Isohara T., Horuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RN Greengard P., Naito A.C., Suzuki T.;
RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT precursor protein at Ser655 by a novel protein kinase.";
RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN [18]
RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP THR-743.
RX MEDLINE=99274744; PubMed=10341243;
RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Naito A.C.,
RN Kirino Y., Greengard P., Suzuki T.;
RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT during neuronal differentiation.";
RL J. Neurosci. 19:4421-4427(1999).
RN [19]
RP PHOSPHORYLATION SITE THR-743.
RX MEDLINE=20396183; PubMed=10936190;

RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greenard P., Kirino Y., Mairn A.C., Suzuki T.,
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [20]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316; DOI=10.1074/jbc.M105818200;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.,
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 RT contains chondroitin sulfate B in the repeating disaccharide region
 RT and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(I) and JIP. Inhibits
 CC G(I) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).

Query Match 88.3%; Score 143; DB 1; Length 770;
 Best Local Similarity 90.0%; Pred. No. 2,4e-12;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGA 30
 Db 672 DAERFHDGSEVHHOKLVFFAEDVGSNKGA 701

RESULT 44
 053ZT3 MOUSE
 ID 053ZT3_MOUSE PRELIMINARY; PRT; 770 AA.
 AC 053ZT3;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Amyloid-beta protein-like protein long isoform.
 GN Name=app;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Szendro P.I., Cadenas C., Eichele G.,
 RT "Sequence of an alternative spliced amyloid-beta precursor protein
 RT homolog.";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; AY267348; AAP23169.1; -, mRNA.
 DR MGI; MGI:88059; APP.
 GO; GO:0016021; C:Integral to membrane; IDA.

DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; ICI.
 SQ SEQUENCE 770 AA; 86552 MW; 26C50DE0890CAFWA CRC64;

Query Match 88.3%; Score 143; DB 2; Length 770;
 Best Local Similarity 90.0%; Pred. No. 2,4e-12;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGA 30
 Db 672 DAERFHDGSEVHHOKLVFFAEDVGSNKGA 701

RESULT 45
 0547B7 RAT
 ID 0547B7_RAT PRELIMINARY; PRT; 770 AA.
 AC 0547B7;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE APP770.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Feng J., Song S., Zheng J.,
 RT "A new beta amyloid precursor protein cDNA found in Rat6 embryo
 RT fibroblasts.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; AF513015; AAM90259.1; -, mRNA.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B8D929A7 CRC64;

Query Match 88.3%; Score 143; DB 2; Length 770;
 Best Local Similarity 90.0%; Pred. No. 2,4e-12;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGA 30
 Db 672 DAERFHDGSEVHHOKLVFFAEDVGSNKGA 701

RESULT 46
 098SF9 XENLA
 ID 098SF9_XENLA PRELIMINARY; PRT; 695 AA.
 AC 098SF9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Beta-amyloid precursor protein B.
 GN Name=app;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21610087; PubMed=11744158; DOI=10.1016/S0169-328X(01)00279-0;
 RA Van den Hurk W.H., Bloemen M., Martens G.J.M.,
 RT "Expression of the gene encoding the beta-amyloid precursor protein
 RT App in Xenopus laevis.";
 RL Brain Res. Mol. Brain Res. 97:13-20(2001).
 [2]

```

RP NUCLEOTIDE SEQUENCE.
RA Van den Hurk W.H.;
RL Thiesen (2001), Department of Biological Sciences, University of
RL Nijmegen, Nijmegen, Netherlands.
DR EMBL, AJ298151, CAC37194.1, -, mRNA.
DR HSSP, Q16019, 1H23.
DR SMR, Q988P9, 27-122, 385-494.
DR GO, GO:0016021, C:integral to membrane; IEA.
DR GO, GO:0005488, F:binding; IEA.
DR InterPro, IPR008155, A4_APP.
DR InterPro, IPR008154, A4_extra.
DR InterPro, IPR001255, Beta-APP.
DR Pfam, PF02177, A4_EXTRA; 1.
DR Pfam, PF03494, Beta-APP; 1.
DR PRINTS, PR00203, AMYLOIDA.
DR PRINTS, PR00204, BETAAMYLOID.
DR SMART, SM00006, A4_EXTRA; 1.
DR PROSITE, PS00319, A4_EXTRA; 1.
DR PROSITE, PS00320, A4_INTRA; 1.
KW Signal.
FT SIGNAL 19 Potential.
SQ SEQUENCE 695 AA; 78803 MW; DC14B02AFB0204A CRC64;

Query Match 86.4%; Score 140; DB 2; Length 695;
Best Local Similarity 80.0%; Pred. No. 6.1e-12;
Matches 24; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 597 DSEYRHDAAYEVHHQKLVFPADVGSNKGA 626

RESULT 47
Q7ZXQ0 XENLA PRELIMINARY; PRT; 695 AA.
ID 07ZXQ0 XENLA PRELIMINARY;
AC Q7ZXQ0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC52816 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodidae; Xenopus; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.W., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Rohak S.A., McEwan P.J., McKernan K.J., Marek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smillie D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA

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RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RL Dev. Dyn. 225:384-391(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC044324, AAH44324.1, -, mRNA.
DR HSSP, Q16019, 1H23.
DR SMR, Q16019, 1H23.
DR GO, GO:0016021, C:integral to membrane; IEA.
DR GO, GO:0005488, F:binding; IEA.
DR InterPro, IPR008155, A4_APP.
DR InterPro, IPR008154, A4_extra.
DR InterPro, IPR001255, Beta-APP.
DR Pfam, PF02177, A4_EXTRA; 1.
DR Pfam, PF03494, Beta-APP; 1.
DR PRINTS, PR00203, AMYLOIDA.
DR PRINTS, SM00006, BETAAMYLOID.
DR SMART, SM00006, A4_EXTRA; 1.
DR PROSITE, PS00319, A4_EXTRA; 1.
DR PROSITE, PS00320, A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78803 MW; C1BD8AAC3356B05 CRC64;

Query Match 86.4%; Score 140; DB 2; Length 695;
Best Local Similarity 80.0%; Pred. No. 6.1e-12;
Matches 24; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGA 30
Db 597 DSEYRHDAAYEVHHQKLVFPADVGSNKGA 626

RESULT 48
Q57394 NARJA PRELIMINARY; PRT; 699 AA.
ID 057394 NARJA PRELIMINARY;
AC 057394;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rf amyloid protein 699.
GN Nemeel ap6599.
OS Nematode japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squales; Hypnosquales; Plistorajea; Batoidae;
OC Torpediniformes; Narkidae; Narkidae; Narkae.
OC NCBI_TaxID=62965;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Electric lobe;
RX MEDLINE=98129705; PubMed=9461486;
RA Iijima K., Lee D.-S., Okutsu U., Tomita S., Hirashima N., Kitano Y.,
RA Suzuki T.,
RT "cDNA isolation of Alzheimer's amyloid precursor protein from
RT cholinergic nerve terminals of the electric organ of the electric
RT ray";
RL Biochem. J. 330:29-33(1998).
DR EMBL, AB005544; BAA24230.1, -, mRNA.
DR HSSP, Q16019, 1H23.
DR SMR, Q57394; 40-135, 136-201, 389-498.
DR GO, GO:0016021, C:integral to membrane; IEA.
DR GO, GO:0005488, F:binding; IEA.
DR InterPro, IPR008155, A4_APP.
DR InterPro, IPR008154, A4_extra.
DR InterPro, IPR001255, Beta-APP.
DR Pfam, PF02177, A4_EXTRA; 1.
DR Pfam, PF03494, Beta-APP; 1.
DR PRINTS, PR00203, AMYLOIDA.
DR PRINTS, PR00204, BETAAMYLOID.
DR SMART, SM00006, A4_EXTRA; 1.

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DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C0309D50E5C CRC64;

Query Match 82.1%; Score 133; DB 2; Length 699;
Best Local Similarity 80.0%; Pred. No. 6.9e-11;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DAEPFHDSGYEVHVKLVFPAEDVGSNKGA 30
DB 601 ETEPQDSGYEVHVKLVFPAEDVGSNKGA 630

RESULT 49
O4RY33 TETNG PRELIMINARY; PRT; 754 AA.
AC O4RY33;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 3 SCAF14978, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00027170001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NC NCB1_TaxID=99883;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Daelva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Kacinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catcolico L., Poulain J., De Bernardis V.,
RA Craud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landel V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Croollus H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG GenomeScope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014978; CAG06699.1; -; Genomic_DNA.
FT NON TER 1 754
FT SEQUENCE 754 AA; 84740 MW; 4A37B051A9FAD777 CRC64;

Query Match 74.1%; Score 120; DB 2; Length 754;
Best Local Similarity 76.7%; Pred. No. 6.6e-09;
Matches 23; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DAEPFHDSGYEVHVKLVFPAEDVGSNKGA 30
DB 656 ETEPQDSGYEVHVKLVFPAEDVGSNKGA 685

RESULT 50
A4 TETPL STANDARD; PRT; 780 AA.
ID A4_TETPL
AC 073683;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE Beta-amyloid protein (Beta-APP) (A-beta)].
GN Name=APP;
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NC NCB1_TaxID=47145;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Villard L., Tassone F., Crnogorac-Jurcovic T., Clancy K., Gardiner K.;
RT "Analysis of pufferfish homologues of the At-rich human APP gene.";
RL Gene 210:17-24(1998).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -!- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF018165; AAC41275.1; -; mRNA.
DR HSSP; P10646; IIRH.
DR SMR; O73683; 29-124, 478-586.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPT1; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SMO0006; A4 EXTRA; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS0279; BPT1_KUNITZ_2; 1.
KW Amyloid; Glycoprotein; Protease inhibitor; Serine protease inhibitor;
KW Signal; Transmembrane.
FT FT 1 18
FT CHAIN 19 780
FT CHAIN
FT CHAIN
FT CHAIN 682 724
FT TORO_DOM 19 711
FT TRANSMEM 712 732
FT TORO_DOM 733 780
FT DOMAIN 323 382
FT SITE 769 772
FT CARBOHYD 560 560
FT DISULFID 327 378
FT DISULFID 336 361
FT SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 74.1%; Score 120; DB 1; Length 780;
Best Local Similarity 76.7%; Pred. No. 6.9e-09;
Matches 23; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DAEPFHDSGYEVHVKLVFPAEDVGSNKGA 30
DB 682 ETEPQDSGYEVHVKLVFPAEDVGSNKGA 711

ID		PRT.	737 AA.
RESULT_51			
A4_FUGRU	STANDARD;		
AC_O93278:			
DT-10-OCT-2003 (Rel. 42,			
DT-10-OCT-2003 (Rel. 42,			
DT-10-MAY-2005 (Rel. 47,			
Dt Alzheimer's disease amyloid A4 protein homolog precursor [Contains: Beta-amyloid protein (beta-Ap) (A-beta)].			
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Neoteleostei; OC Acanttomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; OC Tetradontidae; Tetraodontidae; Takifugu. NCBI_TaxID=31033; [1]			
RN Nucleotide sequence.			
RP MEDLINE=96252138; PubMed=9599080; DOI=10.1016/S0378-1119(98)00032-8; RA Villard L., Tassone F., Cnognograc-Jucevic T., Clancy K., Gardiner K.; RL "Analysis of puffertish homologues of the At-rich human Ap gene"; Gene 210:17-24(1998). CC - FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity). CC - SUBCELLULAR LOCATION: Type I membrane protein. CC - SIMILARITY: Belongs to the APP family. CC - SIMILARITY: Contains 1 BPT/Kuntz inhibitor domain. CC This Swiss-ProT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. ----- DR EMML AP090120; AAA13392.1; -: Genomic_DNA. DR HSP_P10646; iTRH. 440-542. DR SKR_O93279; 29-124. Pufu rubripes. DR Ensemble; SINEUO00000150276; Fugu rubripes. DR InterPro; IPRO08154; A4_ABP. DR InterPro; IPRO01255; Beta-APP. DR InterPro; IPRO02223; Prot_inh_Kunz-m. DR PANTHER; PTIR10083.SF6; Beta-AP; 5. DR Pfam; PF02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta-APP; 1. DR Pfam; PF00104; Kuntlz_BPTI; 1. DR PRINTS; PR00203; AMYLOIDA4. DR PRINTS; PR00759; BASICPASE. DR PRINTS; PR00204; BETAMYOLOID. DR ProDom; PD000222; Prot_inh_Kunz-m; 1. DR SMART; SMO0006; A4_EXTRA; 1. DR SMART; SMO0131; Ku; 1. DR PROSITE; PS00319; A4 EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNTZ_1; 1. DR PROSITE; PS02079; BPTI_KUNTZ_2; 1. KW Amyloid; Glycoprotein; Protease Inhibitor; Serine protease inhibitor; KM Signal; Transmembrane FT SIGNAL 1 18 potential. FT CHAIN 19 737 Alzheimer's disease amyloid A4 protein FT FT 639 681 homology. FT TOPO_DOM 19 668 beta-amyloid protein (potential). FT TRANSHEM 669 688 Extracellular (Potential). FT TOPO_DOM 690 737 Potential. FT DOMAIN 286 344 Cytoplasmic (Potential). FT SITE 300 301 BPTI/Kuntz inhibitor. FT STATE 726 729 Reactive bond. FT CARBOHYD 522 522 Clathrin-binding (by similarity). FT DISULPHID 290 340 N-linked (GLCNAG...) (potential). FT By similarity.			

Query Match

	Best Local Similarity	71.6%	Score 116;	DB 1;	Length 737;
Matches	21;	Conservative	5;	Mismatches	4;
				Indels	0;
				Gaps	

Oy 1 DAEFRHDSGEYVHKQTLVPFAEDVSNGKA 30
Db 639 ETDKRSAGSEYVHQTLVPFADVDNSRGA 668

RESULT 52

Q4S0U4_TETNG
ID Q4S0U4_TETNG PRELIMINARY; PRT; 759 AA.
AC Q4S0U4;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAP14781, whole genome shotgun sequence.
GN ORNames=GSTENG0002591001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OX NCBI_Taxid=99883;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Autry J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mancusi E., Bonneau L., Fischer C., Ozouf-Costaz C., Benoit A.,
RA Meisel S., Jaffe D., Fisher S., Luftalla G., Dosset C., Segurens B.,
RA Desliva C., Salanoubat M., Levy M., Bondet N., Castellano S.,
RA Athouard C., Tubin C., Castel V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Catellio L., Poulain Y., De Bernardis V.,
RA Craud C., Duprat S., Brotier P., Coutanceau J.P., Gony U.,
RA Parra G., Larrier S., Chappe C., McKernan K.O., McEwan F., Bosak S.,
RA Kellis M., Volt I.N., Gulgo R., Zody M.C., Mesirov J.,
RA Landre-Ton K., Birren B., Hubbard C., Kahn D., Robinson-Rechavi M.,
RA Lauder P., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Landier E.S., Weissendbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]

NCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
RL -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC -! SIMILARITY: Contains 1 BPRT/Kunitz inhibitor domain.
DR EMBL; CAAB01014781; CAG05838.1; -! Genomic_DNA.
DR InterPro; IPRO08155; A4_APP.
DR InterPro; IPRO01255; Beta_APP.
DR InterPro; IPRO02223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz-BPTI; 1.
DR PRINTS; PR00203; AMYLGDIA4.
DR PRINTS; PR00759; BASICPRASE.
DR PRINTS; PR00204; BETAPAYLOD.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA_1.
DR SMART; SM00311; KO; 1.
DR PROSITE; PS00349; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 759 AA; 85017 MW; 5EEF9B8BC6C73233 CRC64;

Query Match 71.6%; Score 116; DB 2; Length 759;
Best Local Similarity 70.0%; Pred. No. 2,6e-08;
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGA 30
Db 661 ETDERGAGYEVVHEKLVFFAEDVGSNKGA 690

RESULT 53

Q8U018_BRARE PRELIMINARY; PRT; 357 AA.

ID Q8U018 BRARE PRELIMINARY; PRT; 357 AA.
AC Q8U018;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Putative mebrane protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole embryo;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Mwa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT app gene during embryonic development."
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ15637; CAC85734.1; -, mRNA.
DR HSSP; Q16019; 1HZ3.
DR SMK; Q8U018; 62-170.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETTAMVLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1

SEQ SEQUENCE 357 AA; 40962 MW; 07D99EEF6C55B2D8 CRC64;

Query Match 63.3%; Score 102.5; DB 2; Length 357;
Best Local Similarity 73.3%; Pred. No. 1.2e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGA 30
Db 262 EAERHRS--EVYHOKLVFFAEDVGSNKGA 288

RESULT 54

Q8U018_BRARE PRELIMINARY; PRT; 472 AA.

ID Q8U018 BRARE PRELIMINARY; PRT; 472 AA.
AC Q8U018;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative mebrane protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;

RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT app gene during embryonic development."
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ15637; CAC85733.1; -, mRNA.
DR HSSP; Q16019; 1HZ3.
DR SMK; Q8U018; 177-285.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETTAMVLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1

SEQ SEQUENCE 472 AA; 53787 MW; 24F7128BE3356550 CRC64;

Query Match 63.3%; Score 102.5; DB 2; Length 472;
Best Local Similarity 73.3%; Pred. No. 1.7e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGA 30
Db 377 EAERHRS--EVYHOKLVFFAEDVGSNKGA 403

RESULT 55

Q919E7_BRARE PRELIMINARY; PRT; 612 AA.

ID Q919E7 BRARE PRELIMINARY; PRT; 612 AA.
AC Q919E7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Slavov D.B., Gardiner K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257742; AAF71748.1; -, mRNA.
DR HSSP; Q16019; 1HZ3.
DR SMK; Q919E7; 1-56, 317-425.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_INTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETTAMVLOID.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1

SEQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;

Query Match 73.3%; Score 102.5; DB 2; Length 612;
Best Local Similarity 73.3%; Pred. No. 2.2e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGA 30
Db 517 EAERHRS--EVYHOKLVFFAEDVGSNKGA 543

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RESULT 56
Q72ZT1_BRARE PRELIMINARY; PRT; 678 AA.
ID Q72ZT1_BRARE
AC Q72ZT1
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Amyloid protein a variant 2.
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271746; AAP22958.1; -, mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; Q72ZT1; 29-124, 383-491.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR CO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 678 AA; 76755 MW; 9416378444FD0BC CRC64;

Query Match 63.3%; Score 102.5; DB 2; Length 678;
Best Local Similarity 73.3%; Pred. No. 2.7e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 DAEPHDSGYEVHOKLVFAEDVGSNKG 30
DB 583 EMBERS--EVYHOKLVFAEDVGSNKG 609

RESULT 57
Q6NUZ1_BRARE PRELIMINARY; PRT; 738 AA.
ID Q6NUZ1_BRARE
AC Q6NUZ1
DT 03-JUL-2004 (Tremblrel. 27, Created)
DT 03-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Amyloid beta (A4) protein a.
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Straube R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., Loguélano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paine J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Walling M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerk A., Schen J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC068375; AAF68375.1; -, mRNA.
DR HSSP; Q16019; 1BA4.
DR SMR; Q6NUZ1; 29-124, 443-551.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR CO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KUF_1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 738 AA; 83577 MW; 3A02A6C158AF57B1 CRC64;

Query Match 63.3%; Score 102.5; DB 2; Length 738;
Best Local Similarity 73.3%; Pred. No. 2.7e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 DAEPHDSGYEVHOKLVFAEDVGSNKG 30
DB 643 EMBERS--EVYHOKLVFAEDVGSNKG 669

RESULT 58
Q90W28_BRARE PRELIMINARY; PRT; 738 AA.
ID Q90W28_BRARE
AC Q90W28
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Amyloid protein.
GN Name=appa; Synonyms=app;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF89401; AAK64495.1; -, mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; Q90W28; 29-124, 443-551.

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DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA_1.
DR Pfam; PF03494; Beta-APP_1.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPASE.
DR PRINTS; PR00204; BETRANYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA_1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA_1.
DR PROSITE; PS00320; A4_INTRA_1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SO SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;

Query Match 63.3%; Score 102.5; DB 2; Length 738;
Best Local Similarity 73.3%; Pred. No. 2.7e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGA 30
Db 643 EAERHS---EYHHOKLVFPAEDVSSNKGA 669

RESULT 59
ID Q80U17 BRARE PRELIMINARY; PRT; 239 AA.
AC Q80U17;
DT 01-MAR-2002 (TrEMBLrel. 20. Created)
DT 01-MAR-2002 (TrEMBLrel. 20. Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26. Last annotation update)
DE Putative membrane protein (Fragment).
GN Name=apbb;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole embryo;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Mura A., Lehtsch H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
Dev. Genes Evol. 211:563-567(2001)."
RL EMBL; AJ135638; CAC85735.1; -; mRNA.
DR HSSP; Q16019; IYIT.
DR Ensemble; ENSDARG00000014494; Danio rerio.
DR ZFIN; ZDB-GENE-020220-1; apbb.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP_1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETRANYLOID.
DR PROSITE; PS00320; A4_INTRA_1.
FT NON TER 1
SO SEQUENCE 239 AA; 27048 MW; 8A69F746F821BAE2 CRC64;

Query Match 62.3%; Score 101; DB 2; Length 239;
Best Local Similarity 60.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGA 30
Db 141 DIEERHAGYDVRRKRLMFLAEDVGSNKGA 170

RESULT 60
ID Q5X1Y5 BRARE PRELIMINARY; PRT; 362 AA.
AC Q5X1Y5;
DT 25-OCT-2004 (TrEMBLrel. 28. Created)
DT 25-OCT-2004 (TrEMBLrel. 28. Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28. Last annotation update)
DE Appb protein.
GN Name=apbb;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Alschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
RA Dietchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Caminici P., Prange C.,
RA Rana S.S., Loqueiliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Foley J., Helton E., Kettelman M., Madan A., Kodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywnski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC083534; AAH83534.1; -; mRNA.
DR SMR; Q5X1Y5; 30-93, 88-177.
DR ZFIN; ZDB-GENE-020220-1; apbb.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA_1.
DR Pfam; PF03494; Beta-APP_1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETRANYLOID.
DR SMART; SM00006; A4_EXTRA_1.
DR PROSITE; PS00320; A4_INTRA_1.
SO SEQUENCE 362 AA; 40986 MW; 5F6AC57AD3EDB08A CRC64;

Query Match 62.3%; Score 101; DB 2; Length 362;
Best Local Similarity 60.0%; Pred. No. 2.1e-06;
Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGA 30
Db 264 DIEERHAGYDVRRKRLMFLAEDVGSNKGA 293


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RESULT 61
ID O9UR92 BRARE PRELIMINARY; PRT; 694 AA.
AC O9UR92;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative membrane protein.
GN Name=appb;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Mura A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ15639; CAC85736.1; -; mRNA.
DR HSSP; Q16019; 11YT.
DR SMR; O8UR9; 30-125, 126-191, 400-509.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:Binding; IEA.
DR InterPro; IPR008155; A4_Extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; BETAMYL04.
DR PRINTS; PR00204; BETAMYL04.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 694 AA; 79227 MW; 2803382D11162DC CRC64;

Query Match 62.3%; Score 101; DB 2; Length 694;
Best Local Similarity 60.0%; Pred. No. 4.2e-06;
Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Cy 1 DAERHDSGYEVYHHQKLVFFAEDVGSNKGA 30
Db 596 DIERHNAGYDVDRKRLMFLAEDGSKNGA 625

RESULT 62
ID O97917 BOVIN PRELIMINARY; PRT; 49 AA.
AC O97917;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Amyloid protein (fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2006685; PubMed=10594237; DOI=10.1007/s00359901180;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
RT level of polymorphism in both intron and exon.";
RL Mamm. Genome 10:1142-1145(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Miller R.;

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RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133033; CAB38017.1; -; Genomic DNA.
DR HSSP; Q16019; 11YT.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:Binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYL04.
FT NON_TER 1 49
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;

Query Match 40.7%; Score 66; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 18 VFPAEDVGSNKGA 30
Db 1 VFPAEDVGSNKGA 13

RESULT 63
ID O7NGT4 GLOVI PRELIMINARY; PRT; 545 AA.
AC O7NGT4;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Acetolactate synthase.
GN Name=lvb; OrderedAccession=gl12804;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.
NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC SPRAYN=PCC 7421.
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Miymuro M., Miyashita H., Tsuchiya T.,
RA Sakano M., Matsuno M., Kawashima K., Kishida Y., Kiyokawa C.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:1137-145(2003).
DR EMBL; BA000045; BAC90745.1; -; Genomic DNA.
DR HSSP; P27696; 10ZH.
DR GO; GO:0003984; F:acetolactate synthase activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0030976; F:thiamin pyrophosphate binding; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR004407; Acolac_synthlg.
DR InterPro; IPR000399; TTP_binding.
DR InterPro; IPR011766; TTP_enzyme_C.
DR InterPro; IPR012000; TTP_enzyme_M.
DR InterPro; IPR012001; TTP_enzyme_N.
DR Pfam; PF02775; TTP_enzyme_C; 1.
DR Pfam; PF02775; TTP_enzyme_M; 1.
DR Pfam; PF02776; TTP_enzyme_N; 1.
DR PIRSF; PIRSF00108; Acetolac_syn_1g; 1.
DR PIRSF; PIRSF001370; TTPD_depend_act; 1.
DR PROSITE; PS00187; TTP_ENZYME8; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 545 AA; 59744 MW; E51B1F57ADFB39F5 CRC64;

Query Match 36.7%; Score 59.5; DB 2; Length 545;
Best Local Similarity 32.4%; Pred. No. 5.3;
Matches 12; Conservative 7; Mismatches 7; Indels 11; Gaps 1;

Cy 3 EFRHDSGYEVYHHQKLVFFAEDVGSNK 28
Db 347 EVAHHDGYVPKPKKITYDRLQVGSDDILSDVGAKH 363

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RESULT 64
Q6EX80_9POTV PRELIMINARY; PRT; 182 AA.
ID Q6EX80_9POTV PRELIMINARY; PRT; 182 AA.
AC Q6EX80_9POTV PRELIMINARY; PRT; 182 AA.
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Polypeptide (Fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12216;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Indian B;
RA Garg I., Spezz C., Khurana S., Mukherjee K., Singh M., Valkonen J.;
RL "Characterization of potato virus Y isolates from India."
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Indian B;
RA Spezz C.J.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ495762; CAD2184.1; -; mRNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001592; Poly.coat.
DR Pfam; PF00767; Poly.coat; 1.
KW Capsid protein; Polypeptide.
FT CHAIN 21 >182 coat protein.
FT NON_TER 1
FT TER 182
SQ SEQUENCE 182 AA; 20287 MW; 7E51EC4C3B63F3E CRC64;

Query Match 35.2%; Score 57; DB 2; Length 182;
Best Local Similarity 53.1%; Pred. No. 3.8;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAERHDSGYEVHOKLVFFAEDV---GSNK 28
Db 7 DDEFEPDS-YEVHQQ-----ANDTIDAGGSNK 32

RESULT 65
POLG_PVYCH STANDARD; PRT; 327 AA.
ID POLG_PVYCH STANDARD; PRT; 327 AA.
AC P21294;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Genome polypeptide [Contains: Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)]
DE (Fragment).
OS Potato virus Y (strain Chinese) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12216;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=91016851; PubMed=2216735;
RA Zhou X.R., Fang R.X., Wang C.Q., Mang K.Q.;
RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)."
RT isolate";
RL Nucleic Acids Res. 18:5554-5554 (1990).
RN [2]
RP REVIEW.
RX MEDLINE=21127308; PubMed=11226583; DOI=10.1016/S0168-1702(01)00220-9;
RA Urcuqui-Inchima S., Haenni A.L., Bernardi F.;
RT "Potyvirus proteins: a wealth of functions."
RL Virus Res. 74:157-175(2001);
CC -1- FUNCTION: Coat protein is involved in aphid transmission, cell-to-cell and systemic movement, encapsidation of the viral RNA and in the regulation of viral RNA amplification.
CC -1- FUNCTION: Nuclear inclusion protein B is a RNA-dependent RNA
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CC polymerase that plays an essential role in the virus replication.
CC -1- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate
CC + RNA(n+1).
CC -1- PFM: The viral RNA of potyviruses is expressed as a single
CC polypeptide which undergoes posttranslational proteolytic
CC processing by the main proteinase N1a-pro resulting in the
CC production of at least ten individual proteins (by similarity).
CC -1- SIMILARITY: Belongs to the potyviruses polypeptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X54058; CAJ37993.1; -; Genomic_RNA.
DR PIR; S11435; S11435.
DR InterPro; IPR001592; Poly.coat.
DR InterPro; IPR001205; RNA_pol_P3D.
DR Pfam; PF00767; Poly.coat; 1.
DR Pfam; PF00680; RdRp_1; 1.
KW Capsid protein; Nucleoside triphosphatase; Polypeptide;
KW RNA-directed RNA polymerase; Structural protein; Transferase.
FT CHAIN <1
FT NON_TER 1
FT SITE 61 327 Coat protein (by similarity).
FT SITE 60 61 Cleavage (by N1a-pro) (by similarity).
FT NON_TER 1
SQ SEQUENCE 327 AA; 36868 MW; 8F8355E2DE6F2F18 CRC64;

Query Match 35.2%; Score 57; DB 1; Length 327;
Best Local Similarity 53.1%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAERHDSGYEVHOKLVFFAEDV---GSNK 28
Db 47 DDEFEPDS-YEVHQQ-----ANDTIDAVGNK 72

RESULT 66
Q9DON5_9POTV PRELIMINARY; PRT; 332 AA.
ID Q9DON5_9POTV PRELIMINARY; PRT; 332 AA.
AC Q9DON5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Polypeptide (Fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12216;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ordinary;
RA Inoue-Nagata A.K., Fonseca M.E.N., Lobo T.O.T.A., de Avila A.C.,
RA Monte D.C.;
RT "Analysis of the nucleotide sequence of the coat protein and 3'-
RT untranslated region of two Brazilian potato virus Y isolates."
RL Flotopato. Bras. 26:45-52(2001).
DR EMBL; AF255659; AAG44632.1; -; Genomic_RNA.
DR PIR; A60924; A60924.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001592; Poly.coat.
DR InterPro; IPR001205; RNA_pol_P3D.
DR Pfam; PF00767; Poly.coat; 1.
DR Pfam; PF00680; RdRp_1; 1.
KW Polypeptide.
FT CHAIN <1
FT NON_TER 1
FT SITE 61 327 nuclear inclusion b protein.
FT SITE 60 332 coat protein.
FT NON_TER 1
SQ SEQUENCE 332 AA; 37566 MW; 38E061EB90209D3A CRC64;

Query Match 35.2%; Score 57; DB 2; Length 332;
```

Best Local Similarity 53.1%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAEFRHDSGYEVHHQKLVFPADV---GSNK 28
Db 52 DDEFEPDS-YEVHHQ-----ANDTIDAGGSNK 77

RESULT 67

Q8JPM2_9POTV PRELIMINARY; PRT; 337 AA.
AC Q8JPM2;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Polypeptide (Fragment).

OS Potato virus Y.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_Taxid=12216;

RN NUCLEOTIDE SEQUENCE.

RA Colaricchio A., Elras M., Chaves A.L.R.;

RT "Molecular characterization of a potato virus Y isolated from Solanum

RT palliuncanthum.";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF525081; AAM83091.1; -; mRNA.

DR GO: GO:0019028; C:Viral capsid; IEA.

DR InterPro: IPR001592; Poly_coat.

DR Pfam: PF00767; Poly_coat; 1.

DR Pfam: PF00680; RdRp_1; 1.

KW Polypeptide.

FT CHAIN

FT NON_TER

FT SEQUENCE

337 AA; 38295 MW; EDC58AACCC842P1 CRC64;

Query Match

Best Local Similarity 53.1%; Pred. No. 7.4;

Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAEFRHDSGYEVHHQKLVFPADV---GSNK 28

Db 57 DDEFEPDS-YEVHHQ-----ANDTIDAGGSNK 82

RESULT 68

Q9WG05_9POTV PRELIMINARY; PRT; 365 AA.

AC Q9WG05;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Polypeptide (Fragment).

OS Potato virus Y.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_Taxid=12216;

RN NUCLEOTIDE SEQUENCE.

RA Bhat A.I., Varma A., Pappu H.R., Rajamannar M., Jain R.K., Praveen S.;

RT "Characterization of a potyvirus from eggplant (Solanum melongena) as

RT a strain of potato virus Y by N-terminal serology and sequence

RT relationships.";

RL Plant Pathol. 48:648-654 (1999).

DR EMBL: AF18153; AAD24553.1; -; Genomic_RNA.

DR PIR: A60924; A60924.

DR GO: GO:0019028; C:Viral capsid; IEA.

DR InterPro: IPR001592; Poly_coat

DR InterPro: IPR001205; RNA_Pol_P3D.

DR Pfam: PF00767; Poly_coat; 1.
DR Pfam: PF00680; RdRp_1; 1.
KW Polypeptide.

Qy 1 DAEFRHDSGYEVHHQKLVFPADV---GSNK 28
Db 85 DDEFEPDS-YEVHHQ-----ANDTIDAGGSNK 110

RESULT 69

Q6EX78_9POTV PRELIMINARY; PRT; 182 AA.
AC Q6EX78;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Polypeptide (Fragment).

OS Potato virus Y.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_Taxid=12216;

RN NUCLEOTIDE SEQUENCE.

RA SRRAT=Indian B;

RT "Characterization of potato virus Y isolates from India."

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ951764; CMD42186.1; -; mRNA.

DR GO: GO:0019028; C:Viral capsid; IEA.

DR InterPro: IPR001592; Poly_coat.

DR Pfam: PF00767; Poly_coat; 1.

DR Pfam: PF00680; RdRp_1; 1.

KW Polypeptide.

FT CHAIN

FT NON_TER

FT SEQUENCE

182 AA; 20153 MW; 788AE459D50BDB1 CRC64;

Query Match

Best Local Similarity 53.1%; Pred. No. 7.5;

Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAEFRHDSGYEVHHQKLVFPADV---GSNK 28

Db 7 DDEFEPDS-YEVHHQ-----ANDTIDAGGSNK 32

RESULT 70

Q9WG05_9POTV PRELIMINARY; PRT; 365 AA.

AC Q9WG05;

DT 01-NOV-1999 (Rel. 16, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Genome polypeptide [Contains: P1 protease (N-terminal protein);

DE Helper component protease (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa

DE kDa protein 1 (6kD); Cytoplasmic inclusion protein (EC 3.6.1.1) (CI); 6

DE kDa protein 2 (6kD); Viral genome-linked protein (VPg); Nuclear

DE inclusion protein A (EC 3.4.22.44) (N1-a) (N1a) (N1a-pro) (49 kDa

DE proteinase) (49 kDa-pro); Nuclear inclusion protein B (EC 2.7.7.48)

DE (N1-b) (N1b) (RNA-directed RNA polymerase); Coat protein (CP) 1.

DE Potato virus Y (strain N) (PVY).

CC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 CC Potyvirus.
 CC NCBI_TaxID=12219;
 CC [1]
 CC NUCLEOTIDE SEQUENCE.
 CC MEDLINE=89279275; PubMed=2732709;
 CC Robergla C., Durand-Tardif M., Tronchet M., Boudazin G.,
 CC Ascier-Manifacier S., Casse-Delbart F.,
 CC "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.",
 CC J. Gen. Virol. 70:935-947(1989).
 CC [2]
 CC SEQUENCE REVISION.
 CC Durand-Tardif M.;
 CC Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.
 CC [3]
 CC REVIEW.
 CC MEDLINE=21127308; PubMed=1126583; DOI=10.1016/S0168-1702(01)00220-9;
 CC Ursqui-Inchima S., Haenni A.L., Bernardi F.;
 CC "Potyvirus proteins: a wealth of functions.";
 CC Virus Res. 74:157-175(2001).
 CC -1- FUNCTION: Coat protein is involved in aphid transmission, cell-to-
 CC cell and systemic movement, encapsidation of the viral RNA and in
 CC the regulation of viral RNA amplification.
 CC -1- FUNCTION: Nuclear inclusion protein B is a RNA-dependent RNA
 CC polymerase that plays an essential role in the virus replication.
 CC -1- FUNCTION: Helper component proteinase is required for aphid
 CC transmission and also has proteolytic activity. Interacts with
 CC virions and aphid stylets. Seems to act as suppressor of post-
 CC transcriptional gene silencing (PTGS), a mechanism of plant viral
 CC defense that limits the accumulation of viral RNAs. May have RNA-
 CC binding activity.
 CC -1- FUNCTION: Cytoplasmic inclusion protein has helicase activity. It
 CC may be involved in replication.
 CC -1- FUNCTION: Both 6k peptides are indispensable for virus replication
 CC (by similarity).
 CC -1- FUNCTION: Nuclear inclusion protein A has RNA-binding and
 CC proteolytic activities.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
 CC further restricted by preferences for the amino acids in p6 - p1,
 CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
 CC Glu-|- (Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polypeptide, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -1- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate
 CC + RNA(n+1).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-
 CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the
 CC processing of the polyviral polypeptide.
 CC -1- DOMAIN: The N-terminus of helper component proteinase is involved
 CC in interaction with stylets. The central part is involved in cell-to
 CC interaction with virions and the C-terminus is involved in cell-to
 CC cell movement of the virus.
 CC -1- PTM: VPg is covalently linked to the genomic RNA (By similarity).
 CC -1- PTM: The viral RNA of potyviruses is expressed as a single
 CC polypeptide which undergoes posttranslational proteolytic
 CC processing by the main proteinase N1a-pro resulting in the
 CC production of at least ten individual proteins. The p1 proteinase
 CC and the HC-pro cleave only their respective C-terminal
 CC autocatalytically. 6k1 is essential for proper proteolytic
 CC separation of p3 from CI (By similarity).
 CC -1- SIMILARITY: Belongs to the potyviruses polypeptide family.
 CC -1- SIMILARITY: Contains 1 peptidase C4 domain.
 CC -1- SIMILARITY: Contains 1 peptidase C6 domain.
 CC -1- SIMILARITY: Contains 1 peptidase S30 domain.
 CC -----
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 CC removed.
 CC -----
 CC EMBL, X12456; CAA30988.1; -; Genomic_RNA.

DR EMBL; D00441; BAA00342.1; -; Genomic_RNA.
 DR MEROPS; C04.002; -;
 DR MEROPS; C06.001; -;
 DR MEROPS; S30.001; -;
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR002540; Pept_S30_Poly_P1.
 DR InterPro; IPR001730; Peptidase_C4.
 DR InterPro; IPR001456; Peptidase_C6.
 DR InterPro; IPR001592; Poly_coat.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF002270; DEAD_1.
 DR Pfam; PF002271; Helicase_C_1.
 DR Pfam; PF00863; Peptidase_C4_1.
 DR Pfam; PF00851; Peptidase_C6_1.
 DR Pfam; PF00767; Poly_coat_1.
 DR Pfam; PF01577; Poly_P1_1.
 DR Pfam; PF00680; RDRP_1_1.
 DR PRNTS; PR00966; N1aPOTYPASE.
 DR ATP-Binding; Capsid protein; Covalent protein-RNA linkage; Helicase;
 DR Hydrolyase; Nucleotide-binding; Nucleotidyltransferase; Polypeptide;
 DR Protease; RNA-directed RNA polymerase; Structural protein;
 DR Thiol protease; Transferase.
 DR CHAIN 1 284
 FT CHAIN 285 740
 FT CHAIN 741 1105
 FT CHAIN 1106 1157
 FT CHAIN 1158 1791
 FT CHAIN 1792 1843
 FT CHAIN 1844 2031
 FT CHAIN 2032 2275
 FT CHAIN 2276 2796
 FT CHAIN 2797 3063
 FT NP_BIND 1242 1249
 FT MOTIF 334 337
 FT MOTIF 592 594
 FT MOTIF 1331 1334
 FT MOTIF 1884 1892
 FT ACT_SITE 192 192
 FT ACT_SITE 201 201
 FT ACT_SITE 235 235
 FT ACT_SITE 626 626
 FT ACT_SITE 699 699
 FT ACT_SITE 2077 2077
 FT ACT_SITE 2112 2112
 FT ACT_SITE 2182 2182
 FT BINDING 1907 1907
 FT SITE 284 285
 FT SITE 740 741
 FT SITE 1105 1106
 FT SITE 1157 1158
 FT SITE 1791 1792
 FT SITE 1843 1844
 FT SITE 2031 2032
 FT SITE 2275 2276
 FT SITE 2796 2797
 FT SEQUENCE 3063 AA; 347539 MW; 3EC79125DE33F1BB CRC64;

Query Match 34.0%; Score 55; DB 1; Length 3063;
Best Local Similarity 53.1%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;
Db 1 DAEFRHDSGYEVHHQKLVFPADV---GSNK 28
2783 DDEFELDS-YEVHHQ-----ANDTIDAGSNK 2808

RESULT 71
ID Q8UQ05_9POTV PRELIMINARY; PRT; 3063 AA.
AC Q8UQ05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypotein.
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
NC NCBI_Taxid=12216;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=N-Egypt;
RA Abdel El-Mohsen N.M.A., Gamal El-Dinn A.S., Sobair I.E.-A.,
RT "Characterization of potato virus Y strain 'N-Egypt'.";
RL EMBL: AF522296; AAM81207.1; -; Genomic_RNA.
DR PIR: A60924; A60924.
DR PIR: B46341; B46341.
DR HSSP: P04517; 11VM.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0008026; P:ATP-dependent helicase activity; IEA.
DR GO: GO:0004197; P:Cysteine-type endopeptidase activity; IEA.
DR GO: GO:0003723; P:RNA binding; IEA.
DR GO: GO:0003968; P:RNA-directed RNA polymerase activity; IEA.
DR GO: GO:0006508; P:Proteolysis and peptidolysis; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR GO: GO:0019079; P:Viral genome replication; IEA.
DR InterPro: IPR001410; DEAD/DEAH N.
DR InterPro: IPR001545; Helicase_C.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR002540; Pept_S30_Pcty_P1.
DR InterPro: IPR001592; Pcty_coat.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR InterPro: IPR006662; Thioled.
DR Pfam: PF00270; DEAD_1.
DR Pfam: PF00271; Helicase_C_1.
DR Pfam: PF00863; Peptidase_C4_1.
DR Pfam: PF00851; Peptidase_C6_1.
DR Pfam: PF00767; Pcty_P1_1.
DR Pfam: PF01577; Pcty_P1_1.
DR Pfam: PF00680; RdRP_1_1.
DR PRINTS; PRO0966; N1APOTYPYASE.
DR SMART; SM00487; DEXDC_1.
DR SMART; SM00490; HELIC_1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KM Polypotein.
FT CHAIN 1 224 first component.
FT CHAIN 225 679 helper component.
FT CHAIN 680 1044 third protein.
FT CHAIN 1045 1096 putative 6k1 kD protein.
FT CHAIN 1097 1730 cylindrical inclusion protein.
FT CHAIN 1731 1782 putative 6k2 kD protein.
FT CHAIN 1783 1970 nuclear inclusion-V99.
FT CHAIN 1971 2214 nuclear inclusion-Pro.
FT CHAIN 2215 2736 nuclear protein-b.

FT CHAIN 2737 3002 capsid protein.
SQ SEQUENCE 3063 AA; 347566 MW; A1F1AE8110620EE CRC64;
Query Match 34.0%; Score 55; DB 2; Length 3063;
Best Local Similarity 53.1%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;
Db 1 DAEFRHDSGYEVHHQKLVFPADV---GSNK 28
2783 DDEFELDS-YEVHHQ-----ANDTIDAGSNK 2808

RESULT 72
ID Q56DL4_ROMMI PRELIMINARY; PRT; 687 AA.
AC Q56DL4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hexamerin storage protein 3.
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Romaleidae; Romalea.
NC NCBI_Taxid=7007;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Hachway M.J., Li S., Ding X., Hatle J.D., Borst D.W.;
RT "Molecular characterization of hemolymph storage proteins in the
RT lubber grasshopper";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY63295; AAX62854.1; -; mRNA.
DR SEQUENCE 687 AA; 79785 MW; F1795290C7456F94 CRC64;
Query Match 33.6%; Score 54.5; DB 2; Length 687;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 12; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
Db 8 SGYEVH---OKVFPADVGSNK 28
200 TGTPTATPQKSTFEDVGLNS 223

RESULT 73
ID Q73UH3_MRCPA PRELIMINARY; PRT; 221 AA.
AC Q73UH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=MAP395;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
NC NCBI_Taxid=1770;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: AB017239; AAS05945.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0000271; P:polyaccharide biosynthesis; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007267; GtTA.
DR Pfam: PF04138; GtTA_1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 221 AA; 24838 MW; 9804D0855CFA67CC CRC64;
Query Match 33.3%; Score 54; DB 2; Length 221;
Best Local Similarity 55.6%; Pred. No. 13;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 FRHDSGYEVHOKLVFEFA 21
 DB 79 FRNRGRGRHHEALFFFA 96

RESULT 74
 POLG_PVYVO STANDARD; PRT; 284 AA.

AC P11857;
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Genome polyprotein [Contains: Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)]
 DE (Fragment).
 OS Potato virus Y (strain Y0) (PVY).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
 OC Polyviruses.
 OX NCBI_TaxID=12221;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=89296509; PubMed=2740238;
 RA Bravo-Almonacid F.F., Mentaberry A.N.,
 RT "Nucleotide cDNA sequence coding for the PVY coat protein.";
 RL Nucleic Acids Res. 17:4401-4401(1989).
 RN [2]

REVIEW.

RP MEDLINE=21127308; PubMed=11226583; DOI=10.1016/S0168-1702(01)00220-9;
 RA Urcuqui-Inchima S., Haenni A.L., Bernardi F.;
 RT "Pocytivirus proteins: a wealth of functions.";
 RL Virus Res. 74:157-175(2001).

CC -!- FUNCTION: Coat protein is involved in aphid transmission, cell-to-cell and systemic movement, encapsidation of the viral RNA and in the regulation of viral RNA amplification.
 CC -!- FUNCTION: Nuclear inclusion protein B is a RNA-dependent RNA polymerase that plays an essential role in the virus replication.
 CC -!- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate + RNA(n+1).
 CC -!- PTM: The viral RNA of pocytiviruses is expressed as a single polyprotein which undergoes posttranslational proteolytic processing by the main proteinase N1a-pro resulting in the production of at least ten individual proteins (By similarity).
 CC -!- SIMILARITY: Belongs to the pocytiviruses polyprotein family.

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CC EMBL; X14136; CAA32356.1; -; mRNA.
 DR PIR; S04723; S04723.
 DR InterPro; IPR001592; P0cy_coat.1.
 DR Pfam; PF00767; P0cy_coat.1.
 KW Capsid protein; Nucleosidyltransferase; Polyprotein; Structural inclusion protein B (By similarity); Nuclear inclusion protein B (By similarity); Coat protein (By similarity); Cleavage (by N1a-pro) (By similarity).
 FT CHAIN 18 284
 FT SITE 17 18
 FT NON_TER 1 1
 SQ SEQUENCE 284 AA; 31971 MW; E98535C4607898E2 CRC64;

Query Match 33.3%; Score 54; DB 1; Length 284;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHOKLVFEADV-----GSNK 28
 DB 4 DDEFERDS-YEVVHQ-----ANDTIDAGGNK 29

RESULT 75
 085276_9POTV PRELIMINARY; PRT; 292 AA.

AC 085276;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Polyprotein (Fragment).
 OS Potato virus Y.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
 OC Polyviruses.
 OX NCBI_TaxID=12216;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Griffin J.D., Shiel P.S., Berger P.H., Thornbury D.W.;
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBS databases.
 DR EMBL; M61435; AAA47185.1; -; Genomic_RNA.
 DR PIR; A60924; A60924.
 DR GO; GO:0019028; C:Viral capsid; IRA.
 DR InterPro; IPR001592; P0cy_coat.
 DR Pfam; PF00767; P0cy_coat.1.
 KW Polyprotein.
 FT CHAIN 1 25
 FT NON_TER 26 >292
 FT NON_TER 292 292
 SQ SEQUENCE 292 AA; 32945 MW; 61FE39AF46BF690 CRC64;

Query Match 33.3%; Score 54; DB 2; Length 292;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHOKLVFEADV-----GSNK 28
 DB 12 DDEFERDS-YEVVHQ-----ANDTIDAGGNK 37

RESULT 76
 Y228_BORBU STANDARD; PRT; 971 AA.

AC 051246;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Hypothetical protein BB0228.
 GN OrderedCusNames=BB0228;
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Borrelia burgdorferi group.
 OX NCBI_TaxID=139;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
 RA Frazer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Latifige R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
 RA Swinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
 RA Richardson D.L., Peterson J.D., Kierlavage A.R., Quackenbush J.,
 RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
 RA Gocayne J.D., Weidman J.F., Utterback T.R., Matthey L., McDonald L.A.,
 RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
 RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";
 RL Nature 390:580-586(1997).

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CC EMBL; AE001133; AAC66621.1; -; Genomic_DNA.

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DR PIR; D70128; D70128.
DR TIGR; B80228; 007863; peptidase_M16_C.
DR InterPro; IPR007863; peptidase_M16_C.
DR Pfam; PF05193; peptidase_M16_C_2_protein.
DR Complete Proteome; Hypothetical Protein.
DR SEQUENCE 971 AA; 112960 MW; 0684688DBBC591A CRC64;

Query Match 33.0%; Score 53.5; DB 1; Length 971;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 13; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

OY 1 DAE--FRHDSGYEVHOKLVFPAED 23
DB 19 DAEGYFPGHSGLEVFHKKDSFKEN 44

RESULT 77
ID 022662 ARATH PRELIMINARY; PRT; 195 AA.
AC 022662;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Protein phosphatase U (fragment).
GN Name=PPU;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RP Nucleotide sequence.
RA Horvath D.M., Chua N.-H.;
RE Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC -1- phosphate. Belongs to the PPP phosphatase family.
CC CC
CC EMBL; AF032879; AAA84178.1; -, mRNA.
CC HSPF; 082208; 1M63; Phosphatase activity; IEA.
CC GO; GO:0018787; Phosphatase activity; IEA.
CC InterPro; IPR004813; P_Pesterase.
CC InterPro; IPR006186; P_Putase_sph.
CC Pfam; PF00149; Metallophos; 1.
CC PRINTS; PR00114; STEPHBASE.
CC SMART; SM00156; PP2Ac; 1.
CC Hydroxylase; Icom.
KW NON_TER
FT 1
SQ SEQUENCE 195 AA; 21951 MW; 4B477201BA53BE53 CRC64;

Query Match 32.7%; Score 53; DB 2; Length 195;
Best Local Similarity 56.7%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 7; Indels 6; Gaps 3;

OY 7 DSGYEVHMQ-KL-VFAR--DVGSNKA 30
DB 128 DSGYEVHDKLITVFAPNYCQOMKNKA 157

RESULT 78
ID 09CA59 ARATH PRELIMINARY; PRT; 256 AA.
AC 09CA59;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Putative SPT protein, phosphatase 2A inhibitor; 76220-74135
DE (A1974560/P1M20_24).
DE Name=P1M20_24;
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;

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RN [1]
RP Nucleotide sequence.
RA Lin X., Kaul S., Town C.D., Bentto M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Rinning C.M., Koo H., Fujii C.Y., Uteck T.R.,
RA Bannstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP Nucleotide sequence.
RA Town C.D., Kaul S.;
RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP Nucleotide sequence.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP Nucleotide sequence.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP Nucleotide sequence.
RA EMBL; AC011765; AAG52377.1; -, Genomic DNA.
RA EMBL; AY081733; AAL87386.1; -, mRNA.
RA EMBL; AF385720; AAK60311.1; -, mRNA.
DR PIR; G96774; G96774.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR002164; NAF_family.
DR Pfam; PF00956; NAF; 1.
SQ SEQUENCE 256 AA; 29416 MW; 9DB48574CB1D36FF CRC64;

Query Match 32.7%; Score 53; DB 2; Length 256;
Best Local Similarity 37.0%; Pred. No. 22;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 1 DAEPRHDSGYEVHOKLVFPAEDVGSN 27
DB 192 DAEPRHDSGYEVHOKLVFPAEDVGSN 218

RESULT 79
ID 06RC41 FUSNN PRELIMINARY; PRT; 321 AA.
AC 06RC41;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Cell wall endopeptidase family M23/M37.
DE Ordered locus names=FNO477;
GN Fused bacterium nucleatum (subsp. nucleatum).
OS Fused bacterium nucleatum; Fused bacteriales; Fused bacteriaceae;
OC Bacteria; Fused bacteriales; Fused bacteriales; Fused bacteriales;
OC Fused bacterium.
OC NCBI_TaxID=76856;
RN [1]
RP Nucleotide sequence.
RA STRAIN=ATCC 25586;
RC MEDLINE=21886394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapral V., Anderson I., Ivanova N.,
RA Bhatnagar A., Bartman A., Gardner W.,
RA Vasileva O., Chu L., Kogan Y., Chaga O.,
RA Larsen N., Sousa M., Walunas T., Pusch G.,
RA Fontein M., Kyrpides N.C., Overbeek R.;

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RT "Genome sequence and analysis of the oral bacterium Fusobacterium
GN nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE009951; AAL94673.1; -, Genomic_DNA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR002866; Peptidase_M23B.
DR Pfam; PF01476; LysM; 2.
DR Pfam; PF01551; Peptidase_M23; 1.
DR SMART; SM00257; LysM; 2.
DR Complete proteome.
SQ SEQUENCE 321 AA; 35455 MW; 0E415B802AA52DD9 CRC64;

Query Match 32.7%; Score 53; DB 2; Length 321;
Best Local Similarity 40.0%; Pred. No. 28;
Matches 11; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

OY 5 RHDSGYEVHHQKLVFFAEDVGS--NKG 29
DB 260 KHDNGYETRYAHLSTVSGEHNKG 286

RESULT 80
O7VDP1_PROMA PRELIMINARY; PRT; 339 AA.
AC O7VDP1;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Photosystem II stability/assembly factor.
GN OrderededLocNames=Pro0327;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxId=1219;
RV [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SARG / CMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Attiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weisenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR EMBL; AE017163; AAP9373.1; -, Genomic_DNA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR Pfam; PF02012; BNR; 4.
DR Complete proteome.
SQ SEQUENCE 339 AA; 37498 MW; B9763FC7D161A75D CRC64;

Query Match 32.7%; Score 53; DB 2; Length 339;
Best Local Similarity 40.0%; Pred. No. 30;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 3 EFRHDSGYEVHHQKLVFFAEDVGSN 27
DB 98 DFKEDEGWTVGQPNVLHSEDAKGN 122

RESULT 81
O662D6_BORGA PRELIMINARY; PRT; 972 AA.
ID O662D6;
AC O662D6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

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DE Hypothetical protein.
GN OrderededLocNames=BG0231;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxId=29519;
RV [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB1;
RA Schutte-Spechtel U., Lehmann R., Romwaldt A., Pradella S.,
RA Schutte-Spechtel U., Wilske B., Snelmel J., Platzner M.;
RT "Comparative analysis of the Borrelia garinii genome."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07085.1; -, Genomic_DNA.
DR InterPro; IPR007863; Peptidase_M16_C.
DR Pfam; PF05193; Peptidase_M16_C; 2.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 972 AA; 113320 MW; BD2FEC9279B7562 CRC64;

Query Match 32.7%; Score 53; DB 2; Length 972;
Best Local Similarity 57.9%; Pred. No. 94;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 4 FHRDSGYEVHHQKLVFFAE 22
DB 25 FKHDGSLGVFHLKSDSPKE 43

RESULT 82
O85274_9POTV PRELIMINARY; PRT; 1555 AA.
ID O85274_9POTV;
AC O85274;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein (fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxId=12216;
RV [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O;
RX MEDLINE=92335011; PubMed=1630927;
RA Hidaaka M., Yoshida Y., Maesaki H., Namba S., Yamashita S.,
RA Iwashizaki T., Dozum T.;
RT "Cloning and sequencing of the 3' half of a potato virus Y (O strain)
RT genome encoding the 5k protein, protease, polymerase and coat
RT protein."
RL Nucleic Acids Res. 20:3515-3515(1992).
CC -I- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate
+ RNA(n+1).
DR EMBL; D12539; BAA02107.1; -, Genomic_RNA.
DR PIR; A60924; A60924.
DR PIR; JTO959; JTO959.
DR PIR; PC1072; PC1072.
DR HSSP; P04517; ILVM.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001730; Peptidase_C4.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_Psvir.

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DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00767; Poly_coat; 1.
DR Pfam; PF00680; Rdrp_1; 1.
DR PRINTS; PR00966; N1AP07P7R5R.
KW Capsid protein; Polyprotein; Protease; RNA replication;
KW Structural protein.
FT CHAIN <1 285 cytoplasmic inclusion body.
FT CHAIN 286 337 5-KD protein.
FT CHAIN 338 769 protease.
FT CHAIN 770 1288 RNA polymerase.
FT CHAIN 1289 1555 coat protein.
FT NON_TER 1 1
SQ SEQUENCE 1555 AA; 176935 MW; 86C8C81A29211DE3 CRC64;

Query Match 32.7%; Score 53; DB 2; Length 1555;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 10; Gaps 3;

Qy 1 DAEFRHDSGYEVHHQKLVFPAEDV----GSNK 28
Db 1275 DDEFRFDS-YEVHHQ-----ANDITDAGGK 1300

RESULT 83

OSMW16 LEGPL
ID OSW16 LEGPL PRELIMINARY; PRT; 324 AA.
AC OSW16
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames-Ip11467;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=257245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazale C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Buchrieser C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.,
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity."
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628337; CAH15707.1; -; Genomic_DNA.
DR Legiolist; Ip11467; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR005476; Transketo_C.
DR InterPro; IPR005475; Transketo_Cen_R.
DR Pfam; PF02780; Transketolase_C; 1.
DR Pfam; PF02779; Transket pyr; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 324 AA; 35412 MW; 30C97C19B5724D82 CRC64;

Query Match 32.4%; Score 52.5; DB 2; Length 324;
Best Local Similarity 52.4%; Pred. No. 34;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 10 YEV-HHOKLVFPAEDVGSNKG 29
Db 16 YELAHDENVVVFGEVDVGNKG 36

RESULT 84

OSX504 LEGPA
ID OSX504 LEGPA PRELIMINARY; PRT; 324 AA.
AC OSX504
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DS Hypothetical protein.

GN OrderedLocustNames-Ip11516;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazale C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Buchrieser C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.,
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity."
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628336; CAH12667.1; -; Genomic_DNA.
DR Legiolist; Ip11516; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR005476; Transketo_C.
DR InterPro; IPR005475; Transketo_Cen_R.
DR Pfam; PF02780; Transketolase_C; 1.
DR Pfam; PF02779; Transket pyr; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 324 AA; 35426 MW; 30DBFB89A7F0DD82 CRC64;

Query Match 32.4%; Score 52.5; DB 2; Length 324;
Best Local Similarity 52.4%; Pred. No. 34;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 10 YEV-HHOKLVFPAEDVGSNKG 29
Db 16 YELAHDENVVVFGEVDVGNKG 36

RESULT 85

Q52V81 LEGPH
ID Q52V81 LEGPH PRELIMINARY; PRT; 324 AA.
AC Q52V81
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Pyruvate dehydrogenase E1 beta subunit (EC 1.2.4.1).
GN OrderedLocustNames-Ip91559;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15442721; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Aksamit G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.U.,
RA Seshenko V., Park S.H., Zhao B., Tepiltskaya E., Edwards J.R.,
RA Pampou S., Georgioulou A., Chou I.-C., Iannicelli W., Uiz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.,
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila."
RL Science 305:1966-1968(2004).
DR EMBL; AB017354; AAU27641.1; -; Genomic_DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004739; F:pyruvate dehydrogenase (acetyl-transferring. . .; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR005476; Transketo_C.
DR InterPro; IPR005475; Transketo_Cen_R.
DR Pfam; PF02780; Transketolase_C; 1.
DR Pfam; PF02779; Transket pyr; 1.
KM Complete proteome; Oxidoreductase; Pyruvate.
SQ SEQUENCE 324 AA; 35426 MW; 30DBFB89A7F0DD82 CRC64;

Query Match 32.4%; Score 52.5; DB 2; Length 324;

Best Local Similarity 52.4%; Pred. No. 34;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 10 YEV-HHOKLVFPADVGSNK 29
Db 16 YELAHDENVVVFGEVGNKG 36

RESULT 86

OCETO_YARLI
ID OCETO_YARLI PRELIMINARY; PRT; 939 AA.
AC OCETO;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Yarrowia lipolytica chromosome B of strain CL189 of Yarrowia
DE lipolytica.
GN OrderedLocustNames=YALI0B13222g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_taxid=4952;
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla B.,
RA Goffard N., Franquet L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Batray S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boismere A., Boyer J., Cactolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantrepe F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesut I., Ma L., Muller H.,
RA Nicard J.-M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Candron B., Searpelli C., Gallardin C., Weissenbach J.,
RT Wincker P., Souciet J.-L.;
RL "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
DR EMBL; CR382128; CAG83083.1; -; Genomic_DNA.
KM Complete proteome.

SO SEQUENCE 939 AA; 107429 MW; A60824B309593AC CRC64;

Query Match 32.4%; Score 52.5; DB 2; Length 939;

Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 17; Gaps 2;

Qy 1 DAERF-----HDSG-----YEVHHOKLVFPF 22
Db 638 DKERFLSMELISVLDHTIGMTAEEDFKHQRVFPAD 676

RESULT 87

Q6EX79_9POTV
ID Q6EX79_9POTV PRELIMINARY; PRT; 182 AA.
AC Q6EX79;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Polypeptide (Fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_taxid=12216;
RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Indian D;
RA Garg I., Spez C., Khurana S., Mukherjee K., Singh M., Valkonen J.;
RT "Characterization of potato virus Y isolates from India."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Indian D;
RA Spez C.J.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ495763; CAD42185.1; -, mRNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001592; Poty coat.
DR Pfam; PF00767; Poty coat; 1.
KM Capsid protein; Polypeptide.
FT CHAIN 21 >182 coat protein.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 20302 MW; 61B77C9983290E4A CRC64;

Query Match 32.1%; Score 52; DB 2; Length 182;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAERFHDGVEVHHOKLVFPADV---GSNK 28
Db 7 DDERFSDS-YEVHHQ-----ANDTIDAGGSSK 32

RESULT 88

Q6EX81_9POTV
ID Q6EX81_9POTV PRELIMINARY; PRT; 182 AA.
AC Q6EX81;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Polypeptide (Fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_taxid=12216;
RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Indian A;
RA Garg I., Spez C., Khurana S., Mukherjee K., Singh M., Valkonen J.;
RT "Characterization of potato virus Y isolates from India."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Indian A;
RA Spez C.J.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ495761; CAD42183.1; -, mRNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001592; Poty coat.
DR Pfam; PF00767; Poty coat; 1.
KM Capsid protein; Polypeptide.
FT CHAIN 21 >182 coat protein.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 20333 MW; 7700E5A8C6B8C28B CRC64;

Query Match 32.1%; Score 52; DB 2; Length 182;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

Qy 1 DAERFHDGVEVHHOKLVFPADV---GSNK 28
Db 7 DDERFSDS-YEVHHQ-----ANDTIDAGGSSK 32

RESULT 89

Q7DS55_MYCTU
ID Q7DS55_MYCTU PRELIMINARY; PRT; 256 AA.
AC Q7DS55;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.

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GN OrderedLocustNames=MT3377;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
RA Petersmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
RA Frieschmann R.D., Deboy R.T., Dodson R.J., Gwynn M.L., Hatte D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzman S.L., Delcher A., Uettermann T.R., Weidman J.F., Kouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT Laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
DR EMBL; AE000516; AAK47718.1; -; Genomic_DNA.
DR TIGR; MT3377; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007267; Gtra.
DR Pfam; PF04138; Gtra; 1.
DR KEGG; K04138; Gtra; 1.
KM Hypothetical protein.
SQ
Sequence 256 AA; 28422 MW; 877A3063A82AF42A CRC64;

Query Match 32.1%; Score 52; DB 2; Length 256;
Best Local Similarity 55.6%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 FRHDSGYEVHOKLVFPA 21
Db 112 FRDGRGRHRRHALLFPA 129

RESULT 90
P96882_MYCTU PRELIMINARY; PRT; 272 AA.
ID P96882_MYCTU PRELIMINARY;
AC P96882;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE PROBABLE CONSERVED TRANSMEMBRANE PROTEIN.
GN OrderedLocustNames=RV3277;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H37Rv;
RX MEDLINE=8295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigmeier K., Gae S., Barry C.E. III,
RA Tekaita F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Felwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagers K., Krogan K., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
DR EMBL; BX842582; CAB07080.1; -; Genomic_DNA.
DR PIR; F70979; F70979.
DR Tuberculist; RV3277; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.

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DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007267; Gtra.
DR Pfam; PF04138; Gtra; 1.
DR KEGG; K04138; Gtra; 1.
SQ
Sequence 272 AA; 30078 MW; F07597B96A0AB081 CRC64;

Query Match 32.1%; Score 52; DB 2; Length 272;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 FRHDSGYEVHOKLVFPA 21
Db 128 FRDGRGRHRRHALLFPA 145

RESULT 91
Q7TWU2_MYCBO PRELIMINARY; PRT; 272 AA.
ID Q7TWU2_MYCBO PRELIMINARY;
AC Q7TWU2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE PROBABLE CONSERVED TRANSMEMBRANE PROTEIN.
GN OrderedLocustNames=MB3305;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
NCBI_TaxID=1765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Dutfoy S., Grondin S., Lacroix C., Monsenpe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayer R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrett B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX468345; CAD95397.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007267; Gtra.
DR Pfam; PF04138; Gtra; 1.
DR KEGG; K04138; Gtra; 1.
KM Complete proteome; Transmembrane.
SQ
Sequence 272 AA; 30104 MW; E2B597B96A0AB081 CRC64;

Query Match 32.1%; Score 52; DB 2; Length 272;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 FRHDSGYEVHOKLVFPA 21
Db 128 FRDGRGRHRRHALLFPA 145

RESULT 92
Q9EAB7_9POTV PRELIMINARY; PRT; 290 AA.
ID Q9EAB7_9POTV PRELIMINARY;
AC Q9EAB7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Polypeptide (Fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
NCBI_TaxID=12216;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O;
DR Boonham N., Walsh K., Hims M., North J., Barker I.;

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RT "Sequence comparisons within the PVY coat protein highlight a distinct
RT group of recombinant isolates (PVTNT) associated with potato tuber
RT necrotic ringspot disease (PTRND).";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ390306; CAC05618.1; -; Genomic_RNA.
DR PIR; A60924; A60924.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR001592; Pcty_coat.
DR Pfam; PF00767; Pcty_coat; 1.
KM Capsid protein; Polyprotein.
FT CHAIN <1 23 Nib replicase.
FT CHAIN 24 290 coat protein.
FT NON TER 1 1
SQ SEQUENCE 290 AA; 32605 MW; 1566A0BB98FBA36 CRC64;

Query Match 32.1%; Score 52; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

OY 1 DAERHDSGYEVHHQKLVFPADV----GSNK 28
Db 10 DDEFEPDS-YEVHHQ-----ANDTIDAGSSK 35

RESULT 93
O9EAB8_9POTV PRELIMINARY; PRT; 290 AA.
AC O9EAB8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Polypotein (Fragment).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12216;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O;
RA Boonham N., Walsh K., Hims M., North J., Barker I.;
RT "Sequence comparisons within the PVY coat protein highlight a distinct
RT group of recombinant isolates (PVTNT) associated with potato tuber
RT necrotic ringspot disease (PTRND).";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ390305; CAC05617.1; -; Genomic_RNA.
DR PIR; A60924; A60924.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR001592; Pcty_coat.
DR Pfam; PF00767; Pcty_coat; 1.
KM Capsid protein; Polyprotein.
FT CHAIN <1 23 Nib replicase.
FT CHAIN 24 290 coat protein.
FT NON TER 1 1
SQ SEQUENCE 290 AA; 32582 MW; 1563A6DAE4D2A106 CRC64;

Query Match 32.1%; Score 52; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

OY 1 DAERHDSGYEVHHQKLVFPADV----GSNK 28
Db 10 DDEFEPDS-YEVHHQ-----ANDTIDAGSSK 35

RESULT 94
O9EAD1_9POTV PRELIMINARY; PRT; 290 AA.
AC O9EAD1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
OS Potato virus Y.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12216;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O;
RA Boonham N., Walsh K., Hims M., North J., Barker I.;
RT "Sequence comparisons within the PVY coat protein highlight a distinct
RT group of recombinant isolates (PVTNT) associated with potato tuber
RT necrotic ringspot disease (PTRND).";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ390292; CAC05604.1; -; Genomic_RNA.
DR PIR; A60924; A60924.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR001592; Pcty_coat.
DR Pfam; PF00767; Pcty_coat; 1.
KM Capsid protein; Polyprotein.
FT CHAIN <1 290 Nib replicase.
FT CHAIN 24 290 coat protein.
FT NON TER 1 1
SQ SEQUENCE 290 AA; 32624 MW; F6E21A69D432BCB6 CRC64;

Query Match 32.1%; Score 52; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

OY 1 DAERHDSGYEVHHQKLVFPADV----GSNK 28
Db 10 DDEFEPDS-YEVHHQ-----ANDTIDAGSSK 35

RESULT 95
O9USK4_SPOLT PRELIMINARY; PRT; 698 AA.
AC O9USK4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ar1phorin subunit.
GN Name=SL-3;
OS Spodoptera litura (Common cutworm).
OC Eularyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyritinae; Spodoptera.
OX NCBI_TaxID=69820;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fat body;
RA Zheng Y., Yoshiga T., Tojo S.;
RT "cDNA cloning and deduced amino acid sequences of three storage
RT proteins in the common cutworm, Spodoptera litura.";
RL Appl. Entomol. Zool. (Jpn.) 35:31-39 (2000).
DR EMBL; AJ249471; CAB55605.1; -; mRNA.
DR HSSP; P04253; 1ILA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR005203; hemocyanin.
DR InterPro; IPR005204; hemocyanin_N.
DR Pfam; PF03723; Hemocyanin_C; 1.
DR Pfam; PF00372; Hemocyanin_M; 1.
DR Pfam; PF03722; Hemocyanin_N; 1.
DR PRINTS; PR00187; HEMOCYANIN.
DR PROSITE; PS00209; HEMOCYANIN_1; UNKNOWN_1.
DR PROSITE; PS00210; HEMOCYANIN_2; 1.
SQ SEQUENCE 698 AA; 84112 MW; 5F0C17A20A4F757A CRC64;

Query Match 32.1%; Score 52; DB 2; Length 698;
Best Local Similarity 38.5%; Pred. No. 93;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 2 AEFRHDSGYEVHHQKLVFPADVGSN 27

Db 210 ANYNSLSYPNKEQKLSYFEDIDLN 235

RESULT 96

Q5ZPN7_9POTV PRELIMINARY; PRT; 3061 AA.

AC Q5ZPN7; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Polypeptidein.

GN Name=Pol;

OS Potato virus Y.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_TaxId=12216;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=O strain;

RT "Comparison of the genome sequences of PVY isolates with different biological properties.";

RL Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.

RC Barker H., McGeeachy K.D.;

RT biological properties.";

RL Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.

RA Barker H., (Oct-2003) to the EMBL/GenBank/DBJ databases.

RA EMBL; AJ585136; CAB51191.1; Genomic_RNA.

DR GO: GO:0019028; C:Viral capsid; IEA.

DR GO: GO:0005524; F:ATP binding; IEA.

DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.

DR GO: GO:0004157; F:cysteine-type endopeptidase activity; IEA.

DR GO: GO:0003723; F:RNA binding; IEA.

DR GO: GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

DR GO: GO:0006350; P:transcription; IEA.

DR GO: GO:0019079; P:viral genome replication; IEA.

DR InterPro: IPR01410; DEAD.

DR InterPro: IPR01545; DEAD/DEAF_N.

DR InterPro: IPR01650; Helicase_C.

DR InterPro: IPR01730; Peptidase_C4.

DR InterPro: IPR001456; Peptidase_C6.

DR InterPro: IPR002540; Pept_S30_Poly_P1.

DR InterPro: IPR007095; RNA pol DS_PS.

DR InterPro: IPR001205; RNA pol_P3D.

DR InterPro: IPR007094; RNA pol_PSVir.

DR InterPro: IPR00662; Nucleotid.

DR Pfam: PF00270; DEAD. 1.

DR Pfam: PF00271; Helicase_C. 1.

DR Pfam: PF00863; Peptidase_C4; 1.

DR Pfam: PF00881; Peptidase_C6; 1.

DR Pfam: PF00767; Poly_coat. 1.

DR Pfam: PF01577; Poly_P1. 1.

DR Pfam: PF00680; RdRp_1. 1.

DR PRINTS; PR00966; NTPase/PTASE.

DR SMART; SM00480; HELIC_1.

DR PROSITE; PS00194; THIOREDOMIN; UNKNOWN_1.

KA Capsid protein; Polyprotein.

KT CHAIN 1 275 p1.protein.

FT CHAIN 276 740 helper component protein.

FT CHAIN 741 1105 p3.protein.

FT CHAIN 1106 1157 p3.protein.

FT CHAIN 1158 1791 p1.protein.

FT CHAIN 1792 1843 6k2.protein.

FT CHAIN 1844 2031 genome linked protein (VPg).

FT CHAIN 2032 2275 N1b.protein.

FT CHAIN 2276 2794 coat protein.

FT CHAIN 2795 3061 coat protein.

SEQUENCE 3061 AA; 346817 MW; 880EBD29F1329D7A CRC64;

Query Match 32.1%; Score 52; DB 2; Length 3061;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 1; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHOKLVFPAEDV---GSNK 28

Db 2781 DDEFERDS-YEVHNO-----ANDTIDAGSSK 2806

RESULT 97

Q8BYR3_MOUSE PRELIMINARY; PRT; 199 AA.

AC Q8BYR3;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230045D10 product:hypothetical Phosphatidylinositol-specific phospholipase C, X domain containing protein, full insert sequence.

GN Name=Plcx3; Synonyms=B130016010R1k;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CS7BL/6J; TISSUE=Hypothalamus;

RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Akawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giusti C., King B., Kochiwa H., Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schirml L.M., Straubli P., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G., Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.F., Guetlich S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S., Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CS7BL/6J; TISSUE=Hypothalamus;

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CS7BL/6J; TISSUE=Hypothalamus;

RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

```
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nihi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK038575; BAC30052.1; -; mRNA.
DR Ensembl; ENSMUSG0000049148; Mus musculus.
DR MGI; MGI:2442605; B130016010R1X.
DR WGI; WGI:2442605; Plcx3d.
KW Hypothetical protein.
SQ SEQUENCE 199 AA; 23011 MW; 9F699310513C2AE6 CRC64;

Query Match 31.8%; Score 51.5; DB 2; Length 199;
Best Local Similarity 40.7%; Pred. No. 28;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Cy 3 EFRHDSGYE-VHQKLVFPFADVGSNK 28
Db 71 DFNHFYGMQKXHKLVQMLMDIYGNK 97

RESULT 98
O63HM9 HUMAN PRELIMINARY; PRT; 321 AA.
AC O63HM9_
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686J13163.
GN Name=PLCX3; Synonym=DKFZp686J13163;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=uterus endometel;
RG The German cDNA Consortium;
RA Bloeker H., Boeher M., Brandt P., Mewes H.W., Well B., Amid C.,
RA Osanger A., Robo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX648328; CAH56150.1; -; mRNA.
DR Ensembl; ENSG00000182836; Homo sapiens.
DR HGNC; HGNC:31822; PLCXD3.
DR GO; GO:0004629; F:phospholipase C activity; IPA.
DR GO; GO:0007242; P:intracellular signaling cascade; IPA.
```

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DR InterPro; IPR000909; PL_PLC_X.
DR SMART; SM00148; PLCXC; 1.
DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 36300 MW; 8CB2D55B23930B86 CRC64;

Query Match 31.8%; Score 51.5; DB 2; Length 321;
Best Local Similarity 40.7%; Pred. No. 47;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Cy 3 EFRHDSGYE-VHQKLVFPFADVGSNK 28
Db 143 DFNHFYGMQKXHKLVQMLMDIYGNK 169

RESULT 99
O9RPS4 ENTFA PRELIMINARY; PRT; 328 AA.
AC O9RPS4; Q7C312;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE TTP-dependent branched-chain alpha-keto acid dehydrogenase, E1 beta
DE subunit (Branched-chain alpha-keto acid dehydrogenase, E1 component,
DE beta subunit).
GN Name=Bkdb; OrderedLocNames=EF1659;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1951;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=10C1;
RX MEDLINE=99395054; PubMed=10464218;
RA Ward D.E., Ross R.P., Van der Weijden C.C., Snoep J.L., Claiborne A.,
RT "Catabolism of branched-chain alpha-keto acids in Enterococcus
RL J. Bacteriol. 181:5433-5442 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Foute D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Rettlein H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Dougherty S.C., Deboy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RL Enterococcus faecalis."
RL Science 299:2071-2074 (2002).
RX EMBL; AF149712; AAD55378.1; -; Genomic DNA.
DR EMBL; A016952; A081437.1; -; Genomic DNA.
DR HSSP; Q8ZUR7; 1IK6.
DR TIGR; EF1659; -.
DR InterPro; IPR005476; Transketo_C.
DR InterPro; IPR005475; Transketo_Cen_R.
DR InterPro; IPR005014; Transketo_C_Like.
DR Pfam; PF02780; Transketolase_C; 1.
DR Pfam; PF02779; Transket_pyr; 1.
KW Complete proteome.
SQ SEQUENCE 328 AA; 35736 MW; 80D3ED3F70E7D910 CRC64;

Query Match 31.5%; Score 51; DB 2; Length 328;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Cy 15 OKLVFPFADVGSNKG 29
Db 22 EKVVIFSDVGDGKG 36

RESULT 100
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Q41BK7 GIBZE
ID Q41BK7_GIBZE PRELIMINARY; PRT; 344 AA.
AC Q41BK7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG05401.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Altren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gherre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Zander E., graminaeatum genome sequence."
RT "Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CADTTON: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC01000221; EAA73834.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 344 AA; 37927 MW; 24E9A71CD2BD7653 CRC64;

Query Match 31.5%; Score 51; DB 2; Length 344;
Best Local Similarity 64.7%; Pred. No. 60;
Matches 11; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 12 VHHQKLVFADVGSNK 28
DB 247 VHHDKLVF--KDVGVKDK 261

Search completed: April 20, 2006, 10:05:08
Job time : 242 secs